

Family Ties: A Case of Study within Myrtoideae

Benedetta Bernardini¹, Neil Thomas William Ellwood², Simona Ceschin³

^{1,2,3}Department of Science, University of Roma Tre, Viale G. Marconi 446, 00146, Rome, Italy

¹Corresponding Author Email: [benedettabernardini\[at\]libero.it](mailto:benedettabernardini[at]libero.it)

Abstract: *Phylogenetic relationships are important to explain clade evolutionary history, but they are frequently difficult to identify. Myrtaceae family has been shown as potentially good case - study to resolve several phylogenetic questions regarding its family history and evolution. The Myrtaceae (Myrtales order) contains over 5500 species within 144 genera, distributed predominantly in Southern Hemisphere. Several Myrtaceae taxa are known for their economic importance and notable representation in the humid pleotropical forests. The family includes two subfamilies, Psiloxiloideae and Myrtoideae. Interestingly, the Myrtoideae subfamily has a marked disparity in taxa number among its tribes that it has never been explained. Moreover, it includes species with different fruit type (fleshy, dry fruits) and this peculiarity has been previously considered to explain the subfamily diversification, but to no avail. A more highly comprehensive matrix of the BKMMST clade within Myrtoideae was generated and newly analysed. The results showed that considering mainly certain character state (molecular, fruit type, habitus) has been possible provided a new interpretation of family evolution. Fruit types and habitus traits were mapped and different Myrtoideae tribes were spatially and temporally compared. The conclusions represent an added important step to explain the phylogenetic relationships of this complicated family and evaluate a new evolutionary prospective.*

Keywords: Phylogenetic relationship, clade evolutionary history, ancestral character reconstruction, BKMMST clade, Myrtaceae, phylogenetic tree

1. Introduction

The Myrtales is considered the third most species - rich Angiosperm order, with species present in many different habitats, having high flower variety and fruit type (Dahlgren and Thorne 1984). It includes nine families *sensu* APG IV, but most without a clear phylogeny (Dahlgren and Thorne 1984; Stevens 2001; APG IV 2016; Berger et al.2016).

The Myrtaceae is nested within the order and has been intensively studied (Johnson and Briggs 1984; Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010; Thornhill et al.2015). However, only a few morphological factors were assessed initially and occurred in a poor phylogenetic resolution of this moderately sized family (Johnson and Briggs 1984). New taxa and molecular inputs were evaluated, only the main singular Myrtaceae clades were individuated and largely supported (Wilson et al.2001). Although the combination of morphological and molecular information has since resulted in a low congruence between them, several analyses have revealed an intense homoplasy within the family (Gadek et al.1996; Wilson et al.2001, 2005).

The family is composed of about 144 genera and over 5500 species and it is divided into two subfamilies, Psiloxiloideae and Myrtoideae, and 17 tribes (Wilson et al.2005; Wilson 2011). It is distributed predominantly in the Southern Hemisphere (Wilson et al.2001; Biffin et al.2010; Wilson 2011; Thornhill et al.2015), where its taxa occupy a wide range of diverse habitats, from moist tropical and subtropical forests to dry savannahs, from damp - wet to sandy soils and from coastal or lowland to mountain areas (Wilson 2011). The family is particularly well known for its economic importance (e. g. essential oils in *Eucalyptus* spp., several aromatic species in *Syzygium cumini*, edible fruit of *Psidium guajava* and ornamental use of *Callistemon* spp.). The Myrtaceae also represent an important component of humid

tropical forests; they are widely distributed in humid Pleotropical forests, with species and lineage diversity centred in the Australasian region (Craven 2001; Fig.1).

In this family, taxa have either fleshy or dry fruit; consequently, in the past, this distinction was used to manage the taxonomy of the group (McVaugh 1968; Biffin et al.2010). Traditionally, the fleshy fruit character was thought to have originated only once in Myrtaceae evolutionary history, but recently, more data have suggested that this state has multiple, separate origins within the same family (Johnson and Briggs 1984; Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010).

The Myrtaceae is a very old family, placed in the middle - late Cretaceous (Biffin et al.2010; Thornhill et al.2015; Berg et al.2016). Recently, it was shown that plants characterised by a deep - time origin might also display a large disparity in their lineage's taxa number (Nee et al.1992; McPeck and Brown 2007; Ricklefs 2007; Linder 2008; Rabosky 2009; Gehrke and Linder 2011).

The BKMMST group (Backahousieae, Kaniae, Metrosidereae, Myrteae, Syzygieae, Tristanieae tribes) (Biffin et al.2010) forms an interesting clade within the Myrtoideae subfamily, as it represents most of the family diversity (c.3550 species and 68 genera) (WCSP 2020), and it is the only group to encompass fleshy as well as dry fruited taxa. The BKMMST group is composed of very large tribes, such as the Myrteae, estimated at c.2500 species and 51 genera. Syzygieae, a monogeneric tribe with c.1.100 - 1300 species (Parnell et al.2006; WCSP 2020), which contrast severely with very small tribes like Tristanieae, with c.41 species divided into four genera, and Backahousieae, with 13 species and consistent of one genus only (Wilson et al.2005; Harrington et al.2012). To explain the high taxa variation within the family, any potential positive correlations between Myrtoideae's hyper - diverse taxa and

their main characters' innovations have been thoroughly investigated, but in spite of these efforts no successful resolution has been obtained (Moore and Donoghue 2007; Bernardini 2013; Marazzi et al.2019).

Within the Myrtaceae family there are elevated traits of homoplasy and the taxa information freely available are not enough explicit to circumscribe each singular taxon. However, while the family exhibits remarkable life form diversity (Wilson et al.2001; Biffin et al.2010; Wilson 2011; Fahey et al.2019), there is only a limited amount of information about the evolution of the BKMMST traits that might have influenced growth, survival, reproducibility and evolutionary turnover frequencies. To address this shortfall, there is an urgent need for additional information

(morphological, ecological and geographical distribution) on different taxa.

Therefore, in this study, a new collated dataset of the BKMMST clade was examined, which comprised new taxa also from a wider biogeographical area, including Africa, New Caledonia, New Guinea, New Zealand and the Pacific area. The ancestral states of selected characters (fruit type, habitus trait) were reconstructed and geographically mapped. Furthermore, the same data of traits were also used to determine any potential pattern in between these taxa characters, as between the same features and their environmental, geographical distribution.

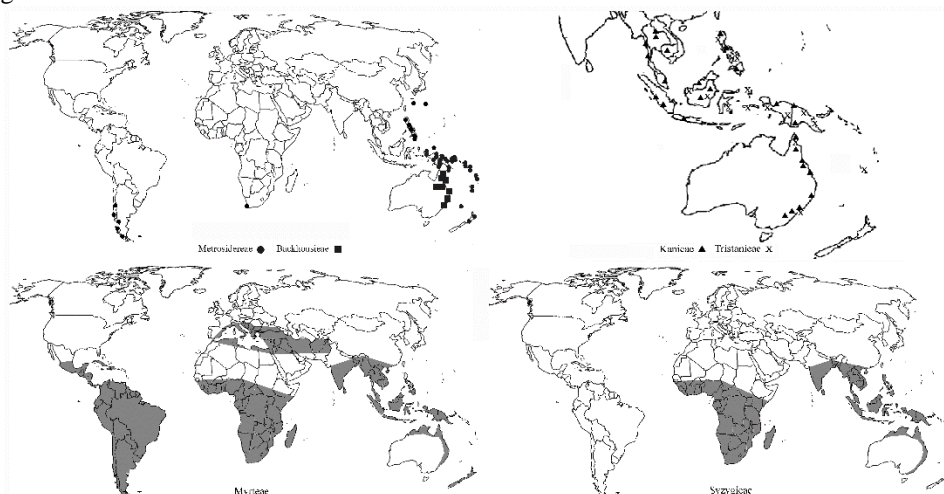


Figure 1: BKMMST clade geographical distribution: a) Metrosidereae and Backhousieae (Mapp by Bernardini 2013); b) Kanieae and Tristanieae (Mapp by Bernardini 2013); c) Myrteae (by Thornhill 2015); d) Syzygieae (by Thornhill 2015)

2. Materials & Methods

2.1 Phylogeny

A new improved matrix that targets specifically the BKMMST clade (Biffin et al.2010) was generated. It was composed of 218 taxa and 6 genes (ETS, ITS, MATK, NDHF, RPL16, PSBA - TRNH; 5418 base pairs). Fifteen taxa were employed as outgroups, because considered closer to the BKMMST cluster (Thornhill et al.2015): *Psiloxylon mauritanium* and *Heteropyxis natalensis*, both taxa in the Psiloxiloideae subfamily; from Myrtoideae, the following taxa were selected: *Xanthostemon chrysanthus* (Xanthostemoineae), *Lophostemon confertus* (Lophostemoneae), *Osbornia octodonta* (Osborneae), *Melaleuca viridiflora*, *Calothamnus validus*, *Beaufortia orbifolia* (Melaleuceae), *Syncarpia glomulifera* (Syncarpieae), *Allosyncarpia ternata*, *Eucalyptopsis papuana*, *Stockwellia quadrifida*, *Arillastrum gummiferum*, *Eucalyptusperriniana*, *Angophora hispida*, and *Corymbia variegata* (Eucalypteae).

Sequences selected in Myrtaceae were aligned using MAFFT v.7.471 (Kato and Standley 2013) and implemented visually in Aliview (Larsson 2014). All the sequences considered were listed in Supporting information S1. Each BKMMST tribe (*sensu* Wilson et al.2005) was fully represented in the resulting dataset with the highest number of genera compared to any previous ones. In this

study, a total of 202 taxa in BKMMST clade were used compared to 63 in Biffin et al. (2010) and 165 BKMMST taxa in Thornhill et al. (2015). Furthermore, the proportions of the selected genera reflected the size of any tribe as well as of the group's geographical distribution.

Each DNA partition was initially evaluated independently by phylogenetic analysis with RAXML v.8 (Stamatakis 2014). Furthermore, to confirm congruence among the genes used in this matrix, the incongruence length difference (ILD) test (Farris et al.1994) was run in PAUP* v.4.0b10 (Swofford 2003) with the following settings: random stepwise sequence addition, TBR branch swapping and 100 replicates. The null hypothesis of congruence was discarded with a threshold of $p < 0.01$ (Li et al.2015).

The final combine matrix was examined with two different evolutionary analyses and three programs: the maximum likelihood (ML) approach and the Bayesian Inference (BI) method. For the first investigation, it was used RAXML v.8 software (Stamatakis 2014) with bootstrap support (BS) and the PhyML vers.3.0 algorithm (Guindon et al.2010), applying a conservative and strong aLTR SH - like support (ALTR). The RAXML analysis was produced through the CIPRES portal (<http://www.phylo.org/subsections/portal/>) with a GTRCAT model and a separate partition for each gene. It was run for 1000 rapid bootstraps, employing the default setting. Meanwhile, the PhyML v.3.0 test was executed on the GITHUB platform (GITHUB.com) with an

SPR heuristic search into the BioNJ starting tree and employing the GTR model of evolution and SH - like branch supports.

For the Bayesian Inference (BI) method, it was used the program MrBayes v.3.2.6 (Ronquist and Huelsenbeck 2003), inclusive of posterior probability (PP) nodes support. The MrBayes was performed through the CIPRES portal, and the best - fitting nucleotide substitution model was estimated for each singular DNA region using Modeltest v.3.7 (Posada and Crandall 1998; Posada and Buckley 2004) under the Akaike information criterion (Akaike 1973). The model selected for each chloroplast is GTR+G; meanwhile, the nuclear genes are under the GTR+G+I model.

In order to approximate the posterior probability distribution, four independent algorithms Markov chain Monte Carlo (MCMC) were run twice for 20 million generations and sampled every 1000th generation with 25% of the 'burn - in' discarded. Convergence between the runs and the length of the burn - in fraction was verified using the "sump" command in MrBayes and Tracer vers.1.5 (Rambaut and Drummond 2009). The posterior distribution of trees was summarised using the half - compact consensus tree from MrBayes. The consensus tree and posterior probability (PP) values were visualised with Figtree vers.1.4 (Rambaut 2012).

In the present study, we considered only parametric and non - parametric node values with high resolution: only BS and ALT values from 85% to 100% and a PP credibility ranging between 0.95 - 1 were assessed as strongly supportive for the phylogenetic relation (Li et al.2015).

All three node' confidences (PP, ALTR, BS) were reported on the phylogenetic tree at tribe level; meanwhile, only the high PP value was displayed at the tips. Furthermore, taxa with conflicting gene resolution (e. g. *Lindsayomyrtus racemoides*, *Syzygium kubiniense* and *Psidium guajava*) were excluded from the analyses.

2.2 DNA extraction

The DNA was extracted from c.0.3 g of silica gel dry material using a modified CTAB extraction protocol of Doyle and Doyle (1997). This was followed by a purification step involving a CsCl - ethidium bromide gradient ultracentrifugation (1.55 g/ml) and dialysis.

Three plastid DNA regions (MATK, NDHF and RPL16) and one nuclear ribosomal DNA region (ITS) were selected and processed (Kew Gardens laboratory). The primers AB101F and AB102F were used for ITS (Douzery et al.1999), XF and 5R for *matK* (www.kew.org/barcoding/), 927F and 2110R for *ndhF* (www.kew.org/barcoding/) and F71 and R1516 for *rpl16* (Shaw et al.2005).

PCR products were purified using the Nucleospin® Extract II minicolumn kit (Macherey - Nagel, Düren), according to the manufacturer's protocol. Sequencing reactions were carried out with the BigDye Terminator vers.3.1 Cycle Sequencing Kit™ (Applied Biosystems Inc.) following the manufacturer's protocol. All amplifications were performed on the GeneAmp 9700 PCD system (Applied Biosystems

Inc.). Sequences were analysed on an ABI 3730 Genetic Analyzer (Applied Biosystems Inc.).

2.3 Time evolution

Calibrating a phylogenetic tree is a fundamental step towards understanding the evolutionary history of lineages, and it is often required as a base for several evolutionary analyses. To understand clearly whether there were any significant age differences in the BKMMST lineages from the main geographical distribution (Neotropics, Australasia and Africa).

The dated phylogeny of the entire matrix (218 taxa) was generated using the real - time algorithm in MEGA vers. X (Kumar et al.2018) and each taxon was coloured in accordance to its geography (Supporting information S2).

2.4 Character state in the BKMMST matrix

The states of selected characters (fruit types, habitus) were described for any taxa included in the current matrix. The relative states for both characters (as reported at the present - time) were plotted on a world map using Tableau 2020.2 (www.tableau.com). A visual comparison between the maps was engaged to report any potential interesting pattern in between the states described. Moreover, it was checked any potential inter - correlation between the characters selected and their geography.

2.5 Ancestral character reconstruction (ACR)

ACR has been widely used to evaluate the evolution of character states along a phylogenetic tree to understand the evolutionary history of biological entities. The most likely ancestral character state was hypothesised at each internal node on the dated phylogenetic tree generated.

Two discrete characters were analysed: fruit types (number of seeds with its mesocarp class) and habitus trait. The future fruit types was used to predict the seeds survival of a specie and its temporal and spatial colonisation ability, while the habitus trait of an adult plant is indicative of its capacity to access light resources and to disperse diaspores. Fruit type states were sourced from the literature (Supporting information S3) and consist of berry (fleshy fruit with many seeds), drupe (fleshy fruit with 1 or 2 seeds), and capsule (dry fruits with many seeds). The habitus states were scored as: Phanerophyte (P), Nanophanerophyte - Phanerophyte (Np - P), Nanophanerophyte (Np), Climbing (Cl), Chamaephyte - Nanophanerophyte (Ch - Np), Hemicryptophyte - Chamaephyte (H - Ch), following the WCSP (2020) list.

ACR was performed in Mesquite vers.3.61 (Maddison and Maddison 2019), selecting the parsimony method option and the unordered state model. The Mesquite program could not include all the taxa (218) from the main matrix; therefore, a subgroup of only 76 taxa was selected. Although, all BKMMST clades, their full geographical distribution and the related character states were represented. The tips of the resulting dated tree were pruned in R program (R Core Team 2020) to preserve the phyla - relations and branch lengths of the taxa. Phylogenetic uncertainty was taken into account

using 1000 cut, dated trees. The ancestral character state hypotheses for each node were shown on the cut ultrametric tree, with the percentage of trees reconstructed for that particular state within the entire 1000 input tree.

3. Results

3.1 Phylogeny

All the reconstructed phylogenetic trees resulted in the same outcome (Fig.2). The BKMMST group was identified by one deep node that was strongly supported (PP = 1, ALTR =

98, BS = 90) and the clade evolved firstly from a Kanieae monophyletic cluster (K). A distinct node was evident between Myrteae and the combined BMST clade (PP = 0.99, ALTR = 98, BS = 84). The BMST clade was also strongly supported (PP = 1, ALTR = 97, BS = 71), and inside this clade, it was possible to distinguish two groups: Syzygieae, which is closely related to Backousieae (PP = 0.99, ALTR = 100, BS = 87) and Metrosiderae, that it is assumed to be closely related to Tristanieae (PP = 1, ALTR = 99, BS = 79). The unplaced Syncarieae (in the outgroups) has been considered closely related to Eucalypteae (BS = 100).

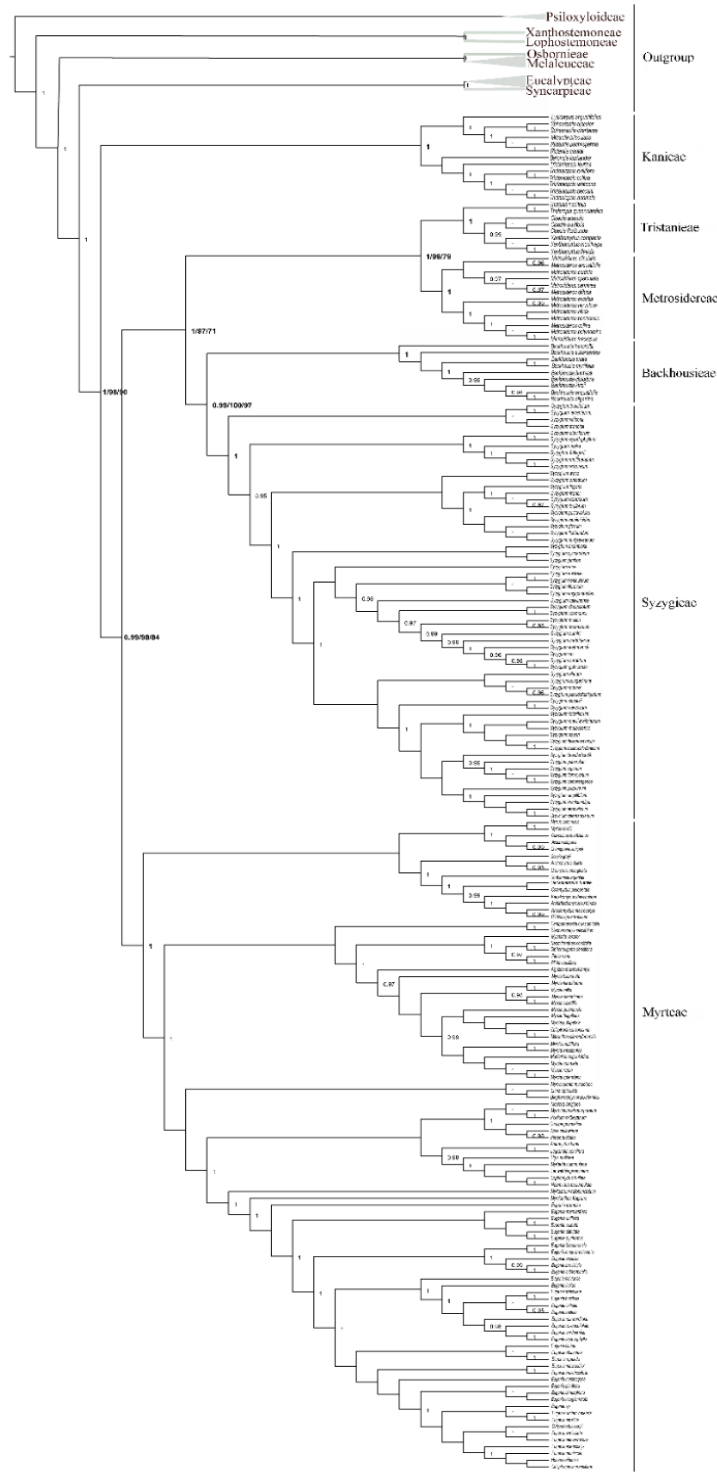


Figure 2: Phylogenetic tree with only high supports at node

BKMMST time in geographical space Tree time analyses suggested Myrteae, Tristanieae and Kaieae to be the oldest tribes, with all their crown nodes estimated at Eocene (Fig.3; S2). Syzygieae and Metrosidereae crown nodes appeared in Oligocene, while the Backhousieae node evolved mainly during the Miocene. A very short origin time occurred in between each singular clade. As a consequence, this particularity might explain difficulties in addressing the

phylogenetic relationships among these monophyletic groups. Most of the BKMMST tribes are centred in Australasia with a few taxa in Africa; only Myrteae taxa are focused in the new world, with some exceptions in Australasia and Africa (Figs.1 and 3; Tab.1).

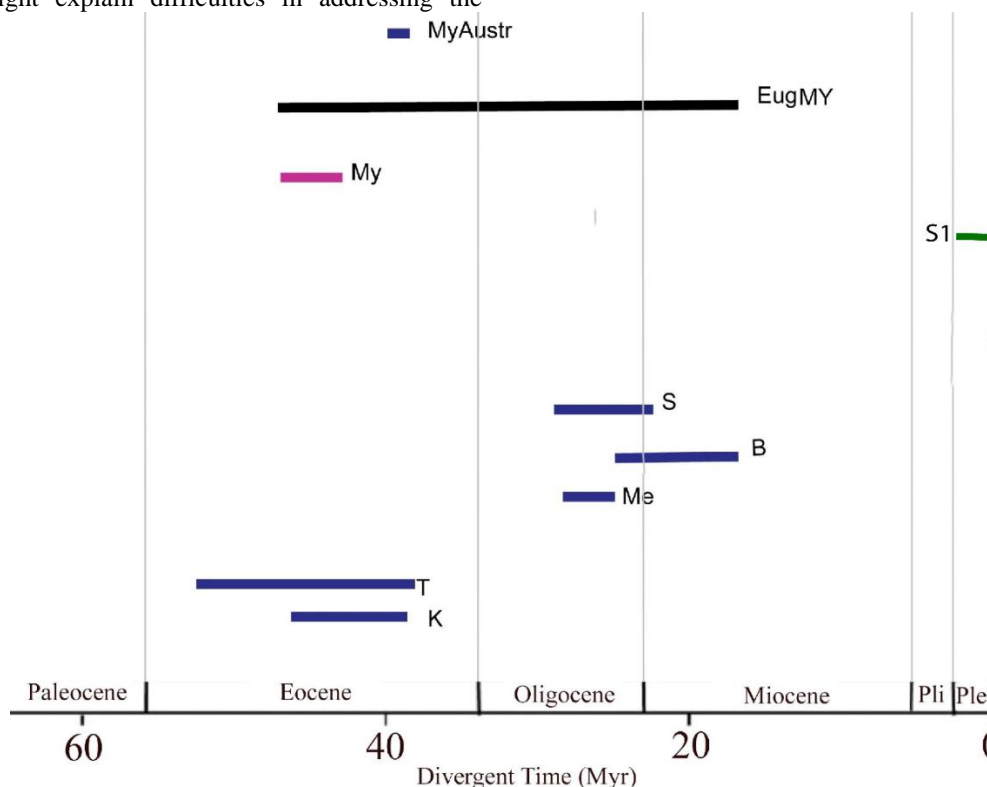


Figure 3: Temporal and geographical origin of BKMMST. Each bar represents a tribe crown age. The nodes are gathered with 95% interval credibility. Neotropics = pink line, Africa = green line, mix origin in South Hemisphere = black line, Southeast Asia = blue line. K = Kanieae, T = Tristanieae, B = Backhousieae, Me = Metrosidereae, S = Syzygieae EastAsia, S1 = Syzygieae in Africa, My = Myrtaceae, My Austr = Australiasin Myrtaceae. The large fleshy - fruited genus *Eugenia* (Myrteae) is highly diversified in South America, with some species in Africa and few in Asia. EugMy = All species of the genus *Eugenia* (Myrteae).

Table 1: Time origin of BKMMST main tribes as retrieved in this paper

| Tribe | Time mean | 95%interval |
|--------------------|-----------|---------------|
| Backhousieae | 20.98 | 15.93 - 25.62 |
| Kanieae | 42.01 | 39.06 - 46.91 |
| Metrosidereae | 29.86 | 25.3 - 30.48 |
| Myrteae | 41.66 | 41.66 - 44.48 |
| Syzygieae | 31.24 | 28.17 - 34.65 |
| Tristanieae | 44.32 | 37.25 - 52.73 |
| Australian Myrteae | 37.13 | 35.63 - 37.15 |
| Eugenia | 27.55 | 17.63 - 44.48 |
| Syzigium_Africa | 1.22 | 0.15/9.88 |

Comparison of fruit and habitus states

Taxa with berry and drupe fruits were shown to have a similar geographical distribution throughout the Southern

Hemisphere, although in south - eastern Asia only drupe fruits were confirmed (Fig.4)

Most of the selected taxa had fleshy fruits, where the drupe type was dominant (97% of all taxa selected), followed by berry (57% of all taxa selected) and then capsular (53% of all taxa selected) fruit types (Fig.4 a).

Of the habitus states across the group, the mixed state of phanerophyte with nanophanerophyte (P - NP, 97%) is the major one, followed by phanerophyte only state (P, 89% of all taxa) and the singular nanophanerophyte only state (Np, 23%), whilst the remaining habitus states was set around 6% of all BKMMST taxa employed (Fig.4 b).

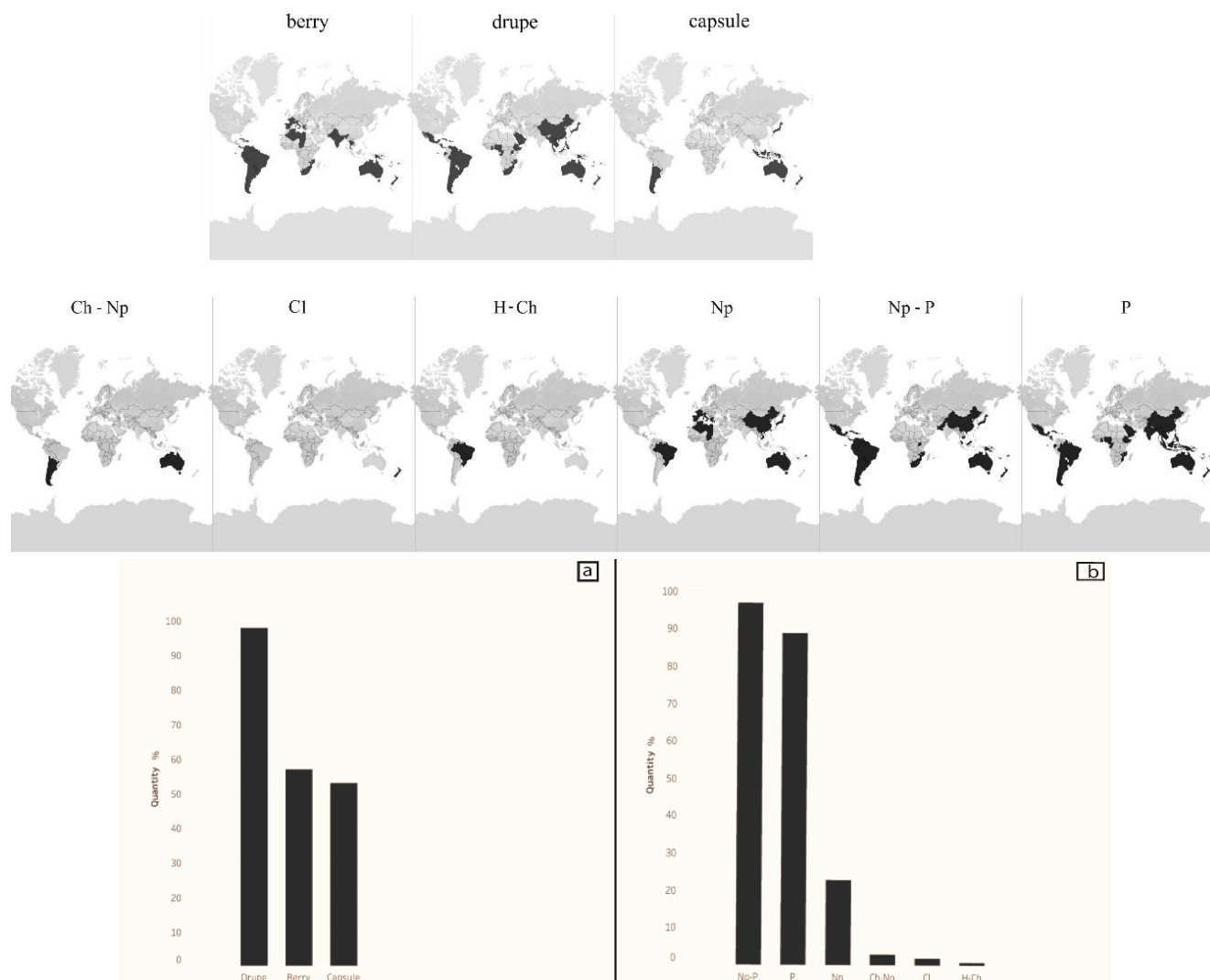


Figure 4: Distribution of fruit type and habitus states in each taxon from the matrix at modern time with character states chart bar. Each state was plotted on a world map (using Tableau 2020.2 by <https://www.tableau.com>). The mapped states of both characters were compared in between to report any potential pattern. The percentage of BKMMST taxa with diverse fruit types (a) and habitus (b). Habitus state codes: Ch= Chamaephyte; Np= Nanophanerophyte; H= Hemicryptophyte; P= Phanerophyte; Cl = Climbing.

ACR - Character evolution fruit type

The capsule fruit type was hypothesised at the origin of BKMMST clade (Fig.5). In the earlier Oligocene, a new fruit state appeared, the berry fruit type, which coexisted with the capsular types through to the earlier Miocene. During the Miocene, the berry fruit type was inherited by many descendant generations, predominantly within the Myrteae. In the Miocene, capsular fruit types were mostly replaced with a novel state, the drupe fruit type, which was mainly dominant in the Syzygieae. In addition, the capsular fruit types were mainly located at the node between Syzygieae and Backahousieae, but the same state was

maintained only in Backahousieae. The capsule status was also inherited and maintained in both the Metrosidereae and Tristanieae. It is interesting to remark the occurrence of the berry fruit inside *Xanthomirtus* taxon (Tristanieae; Wilson et al.2001) because any other taxa in the same tribe are capsular. Kanieae has remained capsular fruits since the Paleocene. In the very early Miocene, drupe fruit also expanded within the Myrteae, simultaneously with the berry type, to become until nowadays the two principal fruit types in this tribe.

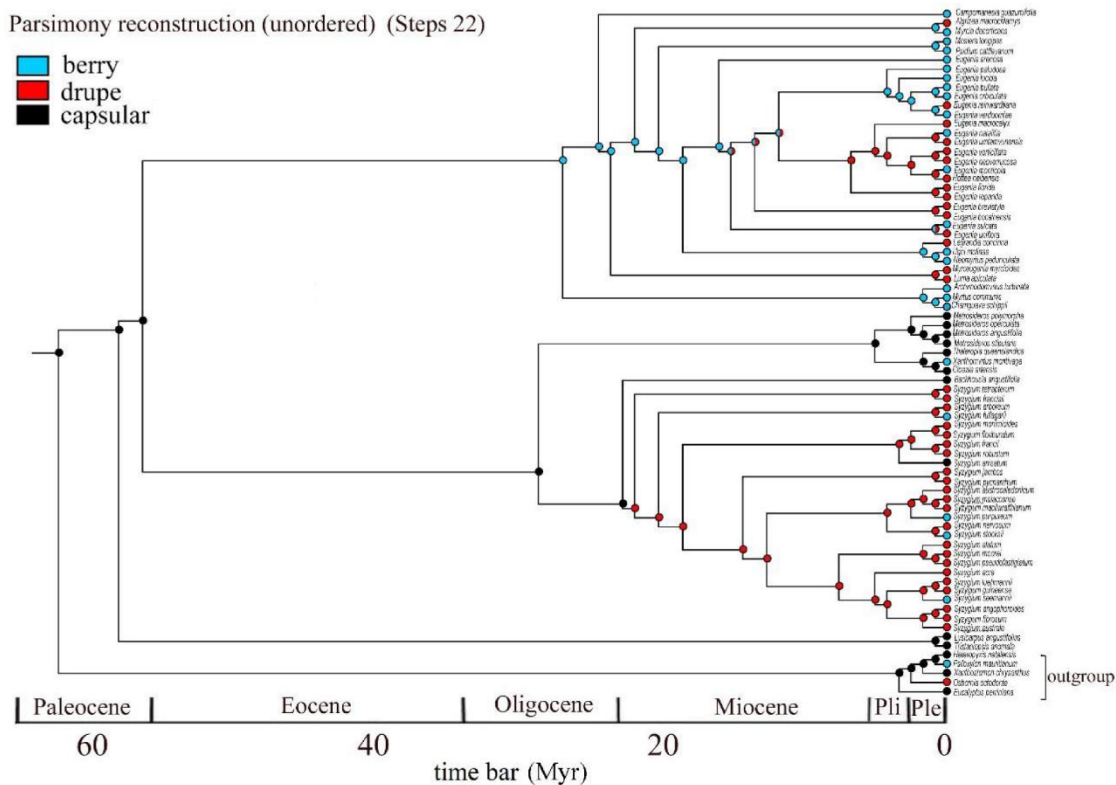


Figure 5: ACR of fruit types in BKMMST with time bar in Myr. Blue dots = Berry; red dots = drupe, black dots = capsule

ACR - Character evolution habitus

The first BKMMST taxa were inferred to be “phanerophyte - only” state, then it has changed into an imprecise status, a mix of phanerophyte or nanophanerophyte, which was assumed to be the main typical BKMMST habitus from late Eocene. The innovative “nanophanerophyte - only” state was found to have occurred only at the tree tips, in nearly all

the tribes, with the singular exclusion of the Tristanieae. Moreover, some lineages were shown to recover the “phanerophyte” state during the Miocene (e. g., most of the Syzygieae and Kanieae taxa). The same state was also retrieved more recently in a few Myrteae and Tristanieae taxa (Fig.6).

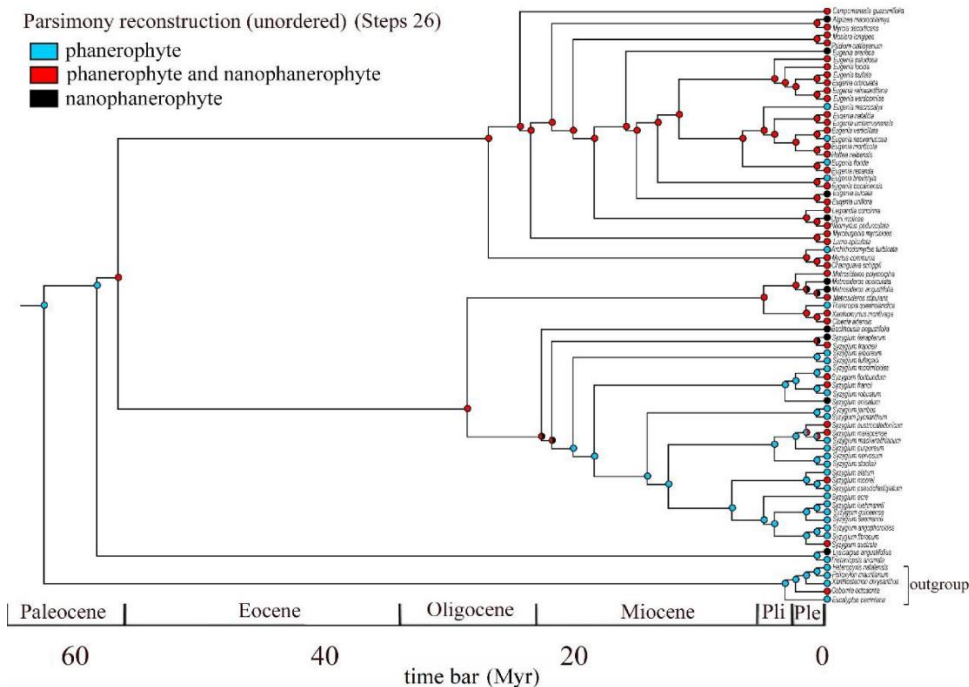


Figure 6: Habitus ancestral reconstruction of BKMMST with time bar in Myr. Blue dot = Phanerophyte; red dot = Phanerophyte and nanophanerophyte; black dot = only nanophanerophyte.

4. Discussion

Phylogeny

For the first time, the BKMMST clade was fully phylogenetically resolved at deep nodes, with each tribe confirmed as monophyletic (Fig.2; Support information S4). Interestingly, it has been noticed that the tribes inside the clade evolved with very short branch length, underling the strong linkage from them. It was thought that the small character differences among these taxa might have been responsible for the many difficulties in producing a completely resolved evolutionary tree for the BKMMST group.

Branches were supported well, according to the non - parametric ALTR and parametric PP values, but often the same nodes had small bootstrap (BS) values. These contrasting confidence results were already identified in previous molecular studies (Biffin et al.2010; Bernardini 2013; Thornhill et al.2015). Differences between ALTR, PP and BS confidences could still indicate a lack of resolution in the evolutionary signal for specific phylogenetic parts (Anisimova et al.2011). As consequence, parametric support may better explain the actual situation.

It was suggested that a low Myrtaceae node support might result from an incomplete sequence coverage of the markers used in older publications (Thornhill et al.2015). Although an impaired gene set was adopted also in this study, the results achieved do not totally confirm the assumption. In most recent studies, it has been stressed that the Myrtaceae cluster received a higher confidence respect to previous molecular investigations (Wilson et al.2001; Sytsma et al.2004; Wilson et al.2005; Biffin et al.2010) as a possible consequence of applying different methodologies (Berget al.2016). Therefore, in this study, a clearer resolution of the controversial clade BKMMST might have been reached because of the better samples proposed and as a possible consequence of the improved analyses used.

Divergence time estimation

Myrtaceae were dated around late Cretaceous (83.6 - 87.5 Ma) (Berg et al.2016), and the extensive fossil records found in Antarctica, Australia, New Zealand, India, Eurasia, North America and South America have suggested that the family had an almost cosmopolitan distribution during and probably prior Eocene. Several recent studies (Sytsma et al.2004, Crisp and Cook 2009) have proposed a massive extinction event in South America that has possibly reduced the number of Myrtaceae taxa, probably because of the family early pantropical distribution.

During the Palaeocene - Eocene era, two important events occurred, the collision between the African and Eurasian plates and the increase in global temperatures, which allowed the expansion of tropical species towards northeaster latitudes. This expansion from the tropics is indicated by the presence of Myrtaceae fossils in Colorado (Manchester et al.1998) and Europe (Collison 1983). In addition, the data suggest that the majority of BKMMST tribes originated during the Eocene, when global temperatures peaked and South America was still connected with Australia across the Antarctica peninsula (Renner et

al.2001; Davies et al.2004). A period of climatic cooling followed, from the end of Eocene to Miocene, forcing the ranges of megathermal taxa to shrink back to lower latitudes into refuge sites such as Central America, Caribbean, East to Southeast Asia and Africa (Richardson et al.2001; Smedmark and Anderberg 2007).

The origin time of the BKMMST clade in Myrtoideae indicated here is consistent with previous studies (Biffin et al.2010; Thornhill et al.2015). It was also demonstrated that the development of each singular clade occurred in very narrow evolutionary timescale (Fig.3; S2). This evolutionary rapidity might explain the difficulties experienced in targeting the phylogenetic relationships among BKMMST clades.

During Miocene and Pliocene, the African forests suffered higher climate oscillations than the Australasian and the Neotropical ecosystems. From c.16 Ma onwards, the southeast African continent experienced uplift and a gradual temperature decrease that could explain an expansion of woodlands and savannah vegetation and a reduction of lowland rainforest (van Zinderen Bakker and Mercer 1986; Jacobs 2004). Generally, the African Myrtoideae groups might have evolved more recently and were characterised by less taxa compared to Australasian and Neotropical clades (e. g. *Eugenia*, *Syzygium*, *Metrosideros*). Such reduction in taxa diversity could be indicative of the unfavourable climate fluctuations during Miocene and Pliocene, which resulted either limited diversification or extinction of older Myrtaceae taxa. Therefore, in tropical area, the taxa diversification often has been explained better as the result of recent dispersal events that are typical of the post - Eocene era (Renner et al.2001; Michalak et al.2010).

Characters evolution

The selected characters generally accumulated changes from the Miocene on (Figs.5 and 6). Previous findings reported a lack of correlation between selected characters with the hyper - taxa diversification of any BKMMST clade. While the fruit types presented highly distinct states, the habitus diverse classes were not so well defined. The character, only phanerophyte is exclusively of tall trees, the state only nanophanerophyte is typical of taxa developing only short trunk, woody bushes or few herbs (Fig.4), but many BKMMST taxa had a mix state, being able to develop either tall or short life forms.

However, here the familial states tested could be linked to ecological attributes, such as climate fluctuation and geological uplift, as resulted by matching this data results with geological era story.

In this paper, it was noted that the BKMMST habitus was characterised by a mix of mainly woody states with tall trees (over 5 m, Phanerophyte) and low trees (less than 5 m, Nanophanerophyte), with only a very few herbaceous species (Fig.6). Normally, large woody life - forms require much more resources than bushes and herbaceous taxa. Here, the results might confirmed that at principle, there were many new environments with abundant resources (nutrients, light), to be colonized. Later on, with advances in evolutionary time, the same supplies availability were

reduced, likely led to a shift from Phanerophyte to mainly Nanophanerophyte plants and more specialist plants, such as Chamaephyte, Hemicryptophyte and Climbing woody life - forms. Furthermore, these results suggested that taxa distribution and resources availability might have been very important for the preservation of older states in Myrtaceae and eventually allowing a faster adaptation to new environmental demands. Syzigieae, focused in Australiasia but the tribe has also expanded into Africa, documented the latter situation clearly. Thus, probably the expansion of this clade into further areas, allowed both the selected traits to preserve the states longer during geological time, displaying a low frequency of character change.

In Angiosperms, a model of phylogenetic niche conservatism has been proposed often, by many researchers and the results obtained in this investigation seemed to support the idea that evolving new adaptations, for a changing environment, is less likely than migrate towards areas with similar ecological niches (Behling et al.2005; Donoghue 2008; Krebs et al.2011). Moreover, the rapid ecological changes (e. g. in climate and geography) occurred during Myrtoideae evolutionary history, could be addressed as responsible for any possible severe extinction event within the clade (Systma et al.2004; Wilson et al.2005; Crisp and Cook 2009).

Traits visualisation

The distributions of the two characters was analysed and it was possible to visualise coexistence between capsular fruits and Chamaephyte and/ or Nanophanerophyte (Ch - Np) life form. Both these features were present just in Australia and in the southern part of South America.

The habitus states which are classified as a mix of Nanophanerophyte and Phanerophyte (Np - P), only Phanerophyte (P) and most of the extant taxa allocated in the only Nanophanerophyte state (Np) were similarly distributed throughout the Southern Hemisphere (Fig.4).

5. Conclusion

The quality data concept was fully adopted in this study, consequentially a new exhaustive taxa sampling of the BKMMST group was analysed. All the clade tribes were represented and new taxa, never adopted before, were added. Each tribe size and its geographical range was considered entirely. The most appropriated BKMMST outgroups and genes were selected, not genuine DNA sequences and informations were discarded as new improved programs were applied.

It was emphasised that the origin time of any examined tribe was very close one each other, so each BKMMST tribe has appeared in a particularly short interval of time. This aspect might explain difficulties in underlining the phylogenetic relationships in the same group.

Wherefore, a new and more exhaustive matrix was evaluated that improved upon previous investigations and new programs were executed, which were more adapted to manage the larger datasets carefully. Hence the matrix resolved into a clearer phylogenetic BKMMST tree.

Finally, dramatic environmental changes, such as global temperature changes (cooling following the early Eocene, or more recent Miocene - Quaternary aridification in Australia and South America (Pole et al.20018), could have shaped Myrtaceae. More in - depth works on the ecological side and further taxa descriptions will be required in the future.

References

- [1] Akaike H.1973. Information theory and an extension of the maximum likelihood principle. Proceedings of 2nd International Symposium on Information Theory. Budapest. Akademia Kiado. p.267–281.
- [2] Anisimova M, Gil M, Ois Dufayard J, Dessimozzi C, Gascuel O.2011. Survey of branch support methods demonstrates accuracy, power, and robustness of fast likelihood - based approximation schemes. Syst Biol.60 (5): 685–699.
- [3] Basinger JF, Greenwood DR, Wilson PG, Christophel DC.2007. Fossil flowers and fruits of capsular Myrtaceae from the Eocene of South Australia. Canad J Bot.85: 204–215.
- [4] Behling H, Pillar V, Bauermann SG.2005. Late Quaternary grassland (Campos), gallery forest, fire and climate dynamics , studied by pollen , charcoal and multi - variate analysis of the São Francisco de Assis core in western Rio Grande do Sul (southern Brazil). Rev Paleobot Palynol.133: 235–248.
- [5] Bell CD, Donoghue MJ.2005. Dating the Dipsacales: comparing models, genes, and evolutionary implications. Am J Bot.92 (2): 284–96.
- [6] Berger BA, Kriebel R, Spalink D, Sytsma KJ.2016. Divergence times, historical biogeography, and shifts in speciation rates of Myrtales. Mol Phylogenet Evol.95: 116–136.
- [7] Bernardini B.2013. Drivers of specification in large fleshy - fruited Myrtaceae genera (*Eugenia* and *Syzygium*). (Dissertation) University of Reading, UK. . Available at <https://ethos.bl.uk/OrderDetails.do?uin=uk.bl.ethos.592664>
- [8] Biffin E, Lucas EJ, Craven LA, Ribeiro da Costa I, Harrington MG, Crisp MD.2010. Evolution of exceptional species richness among lineages of fleshy - fruited Myrtaceae. Ann Bot.106: 79–93.
- [9] Buerki S, Forest F, Alvarez N, Nylander JAA, Arrigo N, Sanmartín I.2011. An evaluation of new parsimony - based versus parametric inference methods in biogeography: a case study using the globally distributed plant family Sapindaceae. J Biogeogr.38: 531–550.
- [10] Collinson ME.1983. Fossil plants of the London Clay. Palaeontological Association Field Guides to Fossils.1. London: The Palaeontological Association.
- [11] Craven LA.2001. Unravelling knots or plaiting rope: What are the major taxonomic strands in *Syzygium* sens. lat. (Myrtaceae) and what should be done with them?. In: Saw LG, Chua LSL, Khoo KC, editors. Proceedings of the 4th Fl. Mal. Symposium on Taxonomy: the cornerstone of biodiversity. Inst. Pen. Perhutanan Malaysia: Kuala Lumpur. p.75–85.
- [12] Crisp MD, Cook LG.2009. Explosive radiation or cryptic mass extinction? Interpreting signatures in molecular phylogenies. Evol Int J Org Evol.63 (9):

- 2257–2265.
- [13] Dahlgren R, Thorne R.1984. The order Myrtales: circumscription, variation, and relationships. *Ann Mo Bot Gard.*71: 633–699.
- [14] Davies TJ, Barraclough TG, Chase MW, Soltis PS, Soltis DE, Savolainen V.2004. Darwin's abominable mystery: Insights from a supertree of the angiosperms. *PNAS.*101 (7): 1904–1909.
- [15] Donoghue JM.2008. A phylogenetic perspective on the distribution of plant diversity. *PNAS* 105: 11549–11556.
- [16] Douzery EJP, Pridgeon AM, Kores P, Linder HP, Kurzweil H, Chase MW.1999. Molecular Phylogenetics of Diseae (Orchidaceae): a contribution from nuclear ribosomal ITS sequences. *Am J Bot.*86 (6): 887–899.
- [17] Doyle JJ, Doyle JL.1997. A rapid DNA isolation procedure from small quantities of fresh leaf tissues. *Phytochemical Bulletin.*19: 11–15.
- [18] Drummond AJ, Rambaut A.2007. BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol Biol.*7, 214: 1–8.
- [19] Fahey M, Rossetto M, Wilson PD, Ho SYW.2019. Habitat preference differentiates the Holocene range dynamics but not barrier effects on two sympatric, congeneric trees (Tristaniopsis, Myrtaceae). *Heredity.*123 (4): 532–548.
- [20] Farris JS, Källersjö M, Kluge AG, Bult C.1994. Testing significance of incongruence. *Cladistics.*10: 315–319.
- [21] Gehrke B, Linder HP.2011. Time space and ecology why some lineages have more species than others. *J Biogeogr* 38: 1948–1962.
- [22] Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O.2010. *Syst Biol.*59 (3): 307–321.
- [23] Harris WK.1965. Basal tertiary microfloras from the Princetown area, Victoria, Australia. *Palaeontographica B.*115: 75–106.
- [24] Harrington MG, Jackes BR, Barrett MD, Craven LA, Barrett RL.2012. Phylogenetic revision of Backhousieae (Myrtaceae): Neogene divergence, a revised circumscription of Backhousia and two new species. *Aust Syst Bot.*25 (6): 409–414.
- [25] Jacobs BF.2004. Palaeobotanical studies from tropical Africa: relevance to the evolution of forest, woodland and savannah biomes. *Philos Trans R Soc B.*359: 1573–1583.
- [26] Johnson LAS, Briggs BG.1984. Myrtales and Myrtaceae – a phylogenetic analysis. *Ann Missouri Bot Gard.*71: 700–756.
- [27] Katoh K, Standley DM.2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.*30: 772–780.
- [28] Krebs U, Park W, Schneider B.2011. Pliocene aridification of Australia caused by tectonically induced weakening of the Indonesian throughflow. *Palaeogeogr, Palaeoclimatol, Palaeoecol.*309 (1–2): 111–117.
- [29] Kumar S, Stecher GLM, Knyaz C, Tamura K.2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Mol Biol Evol.*35 (6): 1547–1549.
- [30] Larsson A.2014. AliView: a fast and lightweight alignment viewer and editor for large datasets. *Bioinform.*30: 3276–3278.
- [31] Li PS, Thomas DC, Saunders RMK.2015. Phylogenetic reconstruction, morphological diversification and generic delimitation of *Disepalum* (Annonaceae). *PLoS One:* 10 e0143481
- [32] Linder HP.2008. Plant species radiations: where, when, why? *Philos Trans R Soc B Biol Sci.*363: 3097–3105.
- [33] Maddison WP, Maddison DR.2019. Mesquite: a modular system for evolutionary analysis. Version 3.61 <http://www.mesquiteproject.org>
- [34] Manchester SR, Dilcher DL, Wing SL.1998. Attached leaves and fruits of myrtaceous affinity from the Middle Eocene of Colorado. *Rev Paleobot and Palynol.*102: 153–163.
- [35] Marazzi B, Gonzalez AM, Delgado - Salinas A, Luckow MA, Ringelberg J, Hughes CE.2019. Extrafloral nectaries in Leguminosae: phylogenetic distribution, morphological diversity and evolution. *Aust Syst Bot.*32: 409–458.
- [36] Mc Peek MA, Brown JM.2007. Clade age and not diversification rate explains species richness among animal taxa. *Am Nat.*169: 97–106.
- [37] McVaugh R.1968. The genera of American Myrtaceae – an interim report. *Taxon* 17: 354–418.
- [38] Michalak I, Zhang LB, Renner SS.2010. Trans - Atlantic, trans - Pacific and trans - Indian Ocean dispersal in the small Gondwanan Laurales family Hernandiaceae. *J Biogeog.*37: 1214–1226.
- [39] Moore BR, Donoghue, MJ.2007. Correlates of diversification in the plant clade Dipsacales: geographic movement and evolutionary innovations. *Am Nat.*170: 28–55.
- [40] Nee S, Mooers AO, Harvey PH.1992. Time and mode of evolution revealed from molecular phylogenies. *PNAS.*89: 8322–8326.
- [41] Oskolski AA, Feng, XX, Jin JH.2013. Myrtineoxylon gen. nov.: The first fossil wood record of the tribe Myrteae (Myrtaceae) in eastern Asia. *Taxon* 62: 771–778.
- [42] Parnell JAN, Craven LA, Biffin E.2006. Matters of scale: dealing with one of the largest genera of angiosperms. In: Hodkinson TR, Parnell JAN. eds. *Reconstructing the Tree of Life: taxonomy and systematics of species rich taxa.* London: CRC Press, 251–274.
- [43] Pole M, Dawson J, Denton T.2008. Fossil Myrtaceae from the Early Miocene of southern New Zealand. *Aust J Bot.*56 (1): 67–81.
- [44] Posada D, Buckley T.2004. Model selection and model averaging in phylogenetics: advantages of Akaike information criterion and Bayesian approaches over likelihood ratio tests. *Syst Biol.*53: 793–808.
- [45] Posada D, Crandall KA.1998. MODELTEST: Testing the model of DNA substitution. *Bioinform.*14: 817–818.
- [46] R Development Core Team.2020. R: A language and environment for statistical computing. Available at: <http://www.r-project.org/>
- [47] Rabosky DL, Lovette IJ.2008. Explosive evolutionary radiations: decreasing speciation or increasing extinction through time? *Evol.*62: 1866–1875.

- [48] Rabosky DL.2009. Ecological limits on clade diversification in higher taxa. *Am Natur.*173: 662–674.
- [49] Rambaut A, Drummond AJ.2009. Tracer, version 1.5. Available at <http://beast.bio.ed.ac.uk/Tracer>
- [50] Rambaut A.2012. FigTree v1.4 software. Available at <http://tree.bio.ed.ac.uk/software/figtree/>
- [51] Renner SS, Clausing G, Meyer K.2001. Historical biogeography of Melastomataceae: the roles of Tertiary migration and long - distance dispersal. *Am J Bot.*88: 1290–1300.
- [52] Richardson JE, Pennington RT, Pennington TD, Hollingsworth PM.2001. Rapid diversification of a species - rich genus of neotropical rain forest trees. *Science* 293: 2242–2245.
- [53] Ricklefs RE.2007. History and diversity: explorations at the intersection of ecology and evolution. *Am Nat.*170: 56–70.
- [54] Ronquist F, Huelsenbeck J.2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinform.*19: 1572–1574.
- [55] Shaw J, Lickey EB, Beck JT, Farmer SB, Liu W, Miller J, Kunsiri C, Siripun C, Winder CT, Schillings EE, Small RL.2005. The tortoise and the Hare II: relative utility of 21 non - coding chloroplast DNA sequences for phylogenetic Analysis. *Am J Bot.*92 (1): 142–166.
- [56] Smedmark JE, Anderberg AA.2007. Boreotropical migration explains hybridization between geographically distant lineages in the pantropical clade Sideroxyloae (Sapotaceae). *Am J Bot.*94 (9): 1491–1505.
- [57] Stamatakis A.2014. RAxML version 8: a tool for phylogenetic analysis and post - analysis of large phylogenies. *Bioinform.*30 (9): 1312–1313.
- [58] Stevens PF. (2001 onwards). Angiosperm Phylogeny Website. Version 14, July 2017 Available at <http://www.mobot.org/MOBOT/research/APweb/>. Accessed July 2019
- [59] Swofford DL.2003. PAUP*. Phylogenetic Analysis Using Parsimony (*and Other Methods). Version 4. Sinauer Associates, Sunderland, Massachusetts, USA.
- [60] Sytsma KJ, Litt A, Zjhra ML, Pires JC, Nepokroeff M, Conti E, Walker J, Wilson PG.2004. Clades, clocks, and continents: historical and biogeographical analysis of Myrtaceae, Vochysiaceae, and relatives in the Southern Hemisphere. *Int. J. Plant Sci.*165: 85–105.
- [61] Tamura K, Battistuzzi FU, Billing - Ross P, Murillo O, Filipinski A, Kumar S.2012. Estimating divergence times in large molecular phylogenies. *PNAS.*109: 19333–19338.
- [62] Tamura K, Qiqing T, Kumar S.2018. Theoretical foundation of the real - time method for estimating divergence times from variable evolutionary rates. *Molecular Biology and Evol.*35: 1770–1782.
- [63] Tarran M, Wilson PG, Macphail MK, Jordan GJ, Hill RS.2017. Two fossil species of *Metrosideros* (Myrtaceae) from the Oligo - Miocene Golden Fleece locality in Tasmania, Australia. *Am J Bot.*104 (6): 891–904.
- [64] The Angiosperm Phylogeny Group (APG).2016. An update of the Angiosperm Phylogeny Group classification of the orders and families of flowering plants: APG IV. *Bot J Linn.*181: 1–20.
- [65] Thornhill AH, Ho SYW, Külheim C, Crisp MD.2015. Interpreting the modern distribution of Myrtaceae using a dated molecular phylogeny. *Mol Phylogenet Evol.*93: 29–43.
- [66] van Zinderen Bakker EM, Mercer JH.1986. Major late Cenozoic climatic events and palaeoenvironmental changes in Africa viewed in a worldwide context. *Palaeogeogr, Palaeoclimatol, Palaeoecol.*56: 217–235.
- [67] WCSP (2020). World Checklist of Selected Plant Families. Facilitated by the Royal Botanic Gardens, Kew. Available at <http://wmsp.science.kew.org/> Accessed February 2020.
- [68] Wilson PG, O'Brien MM, Gadek PA, Quinn CJ.2001. Myrtaceae revisited: a reassessment of infrafamilial groups. *Am J Bot.*88: 2013–2025.
- [69] Wilson PG.2011. Myrtaceae. In: Kubitzki K, editor. The families and genera of vascular plants. Vol.10. Flowering plants Eudicots: Sapindales, Cucurbitales, Myrtaceae. Heidelberg: Springer - Verlag; p.212–271.
- [70] Wilson PG, O'Brien MM, Heslewood MM, Quinn CJ.2005. Relationships within Myrtaceae sensu lato based on a matK phylogeny. *Plant Syst. Evol.*251: 3–19.
- [71] [https://www.researchgate.net/profile/Benedetta - Bernardini](https://www.researchgate.net/profile/Benedetta-Bernardini)
- [72] [https://www.researchgate.net/profile/Simona - Ceschin](https://www.researchgate.net/profile/Simona-Ceschin)
- [73] [https://www.researchgate.net/profile/Neil - Ellwood - 2](https://www.researchgate.net/profile/Neil-Ellwood-2)
- S2 - Molecular dating. Calibration points table and phylogenetic dated tree.
A correct estimation of molecular evolution rates among gene regions and lineages is important to reduce bias effect on age inference (Bell & Donoghue, 2005; Mulchay *et al.*, 2012).
- At first, the dating BEAST approach (Drummond & Rambaut, 2007), which does not assume rate autocorrelation among lineages, was also used. Although it was run several times with different settings, it failed each time to reach convergence and produce acceptable effective sample sizes (ESS). Similar problems were reported by other authors (eg. Buerki *et al.*, 2011), where the size and complexity of the data set was assumed to be the main reason for these failures.
- In this study, the failure of the program BEAST might be explained by the presence of high variable mutation rates, probably very different between the markers used and the large number of taxa employed. Therefore, more versatile dating programs are needed, to better fit datasets characterised by high substitution rates (Rabosky *et al.*, 2008).
- In this scenario, a fast and reliable dating algorithm is real time implemented in MEGA v. X (Kumar *et al.*, 2018). This software allowed to perform complicate analyses, transforming relative node ages into absolute times using calibration records.
- A time - tree was inferred by applying the RelTime method (Tamura *et al.*, 2012, 2018) to the resulting supplied

phylogenetic tree whose branch lengths were calculated using the Maximum Likelihood (ML) method and with the General Time Reversible substitution model.

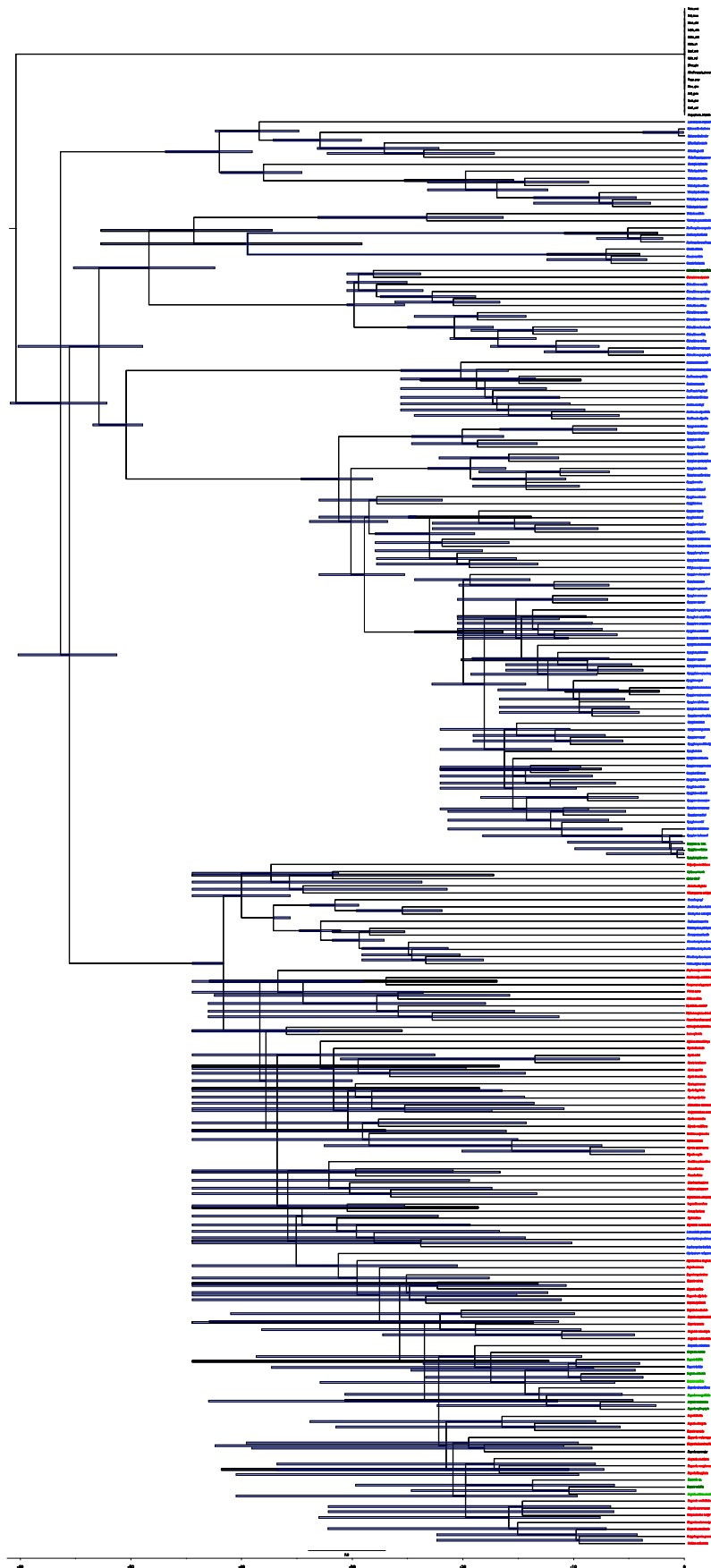
The time - tree was computed using five calibration constraints, setting minimum and maximum time boundaries on nodes (table1). A discrete Gamma distribution model was used to pattern evolutionary rate differences among sites (4 categories, +G). The final dataset consisted in 218 nucleotide sequences with a total of 5418 characters, and codon positions 1st+2nd+3rd+Noncoding, were included.

The phylogenetic tree was dated using five Myrtoideae fossils, and their placements were mostly based on previous studies (Sytsma et al., 2004; Biffin et al., 2010; Thornhill et al., 2015). In order to calibrate Myrteae crown group, the fossil *Myrceugenelloxylon antarcticus* (Rabosky et al., 2008)

was selected and it was estimated Late Cretaceous to Mid - Eocene time. The basal Australian group in Myrteae was recovered, the clade was dated with *Myrtineoxylon maomingensis*, placed in South China, during Late Eocene (Oskolski et al., 2013). The New Zealand fossil spore *Myrtaceidites eugenioides* (Harris et al., 1965) of Early Eocene was used to constrain the nodes connecting Syzygia and Backhousieae. Metrosiderea crown clade was dated during period time from late - oligocene to early Miocene, with several fruit and leaves fossils, recovered in New Zealand (Tarran et al., 2017). *Tristaniandra alleyii* from the Eocene of South Australia suggest an affinity to tribe Kanieae Basinger et al., 2007 [72]). The calibration information from this study are summarised in table 1. Divergence - time results from the current study were similar to those obtained previously (Biffin et al., 2010, Thornhill et al., 2015).

Calibration points summarise the fossil name, relative time node, the node where the fossil was applied on and the fossil rate.

| Fossil | Time (Myr) | Node | Rates |
|---------------------------------------|-------------|------------------------------|----------------------|
| <i>Tristandria alleyi</i> . | 48.6 - 40.4 | Kanieae crown | Uniform distribution |
| <i>myrceugenelloxylon antarcticus</i> | 99.6 - 37.2 | Myrtea crown | Uniform distribution |
| Fruits and leaves | 31.5 - 19 | Metrosiderea crown | Uniform distribution |
| <i>Myrteloxylon maomingensis</i> | 37.2 - 33.9 | Australian Myrteae crown | Uniform distribution |
| <i>myrtaceidites eugenioides</i> | 55.8 - 48.6 | Backhousieae+ Syzygiae crown | Uniform distribution |



Dated tree with color tips names. Red= South America, Blue=East Asia, Green=Africa. Bars on node represent 95% credibility intervals. Geographical area from WCSP, 2020. Time in Myr.

S1 - Taxa used with vouchers and accession number for each gene. Slash symbols indicated no molecular data adopted.

| TAXA | ITS | MATK | NDHF | RPL16 | ETS | TRNH - PSBA | Voucher |
|--|---------------|---------------|---------------|---------------|----------|-------------|--|
| <i>Acca sellowiana</i> (O. Berg) Burret | AM489973 | AY498783 | – | – | AM234067 | – | – |
| <i>Accara elegans</i> (DC.) Landrum | MF954013 | MF954518 | MF954431 | NF954309 | – | MF954271 | – |
| <i>Algrizea macrochlamys</i> (DC.) Proença & Nic Lugh. | AM489976 | – | – | – | AM234126 | – | – |
| <i>Allosyncarpia ternata</i> S. T. Blake | AF390446 | KC180806 | KC180806 | KC180806 | DQ352477 | AF190370 | – |
| <i>Amomyrtus luma</i> (Molina) D. Legrand & Kausel | AM234073 | KM065323 | MF954434 | – | AM489892 | AM489811 | – |
| <i>Angophora hispida</i> (Sm.) Blaxell | KM065051 | KM065116 | – | – | KT631415 | – | – |
| <i>Archirhodomyrtus turbinate</i> (Schltr.) Burret | MF954015 | – | MF954435 | MF954312 | – | MF954273 | – |
| <i>Arillastrum gummiferum</i> (Brongn. & Gris) Panch. exBaill. | AF058454 | AF368198 | AY498765 | – | DQ352479 | – | – |
| <i>Austromyrtus dulcis</i> (C. T. White) L. S. Sm. | MF954016 | AM489977 | MF954436 | – | AM489894 | MH587032 | – |
| <i>Backhousia angustifolia</i> F. Muell | KC134136 | KM894680 | – | – | – | KM895200 | – |
| <i>Backhousia bancroftii</i> F. M. Bailey & F. Muell. | KC134137 | KC134162 | – | – | – | KC134150 | – |
| <i>Backhousia citriodora</i> F. Muell | KM064898 | KM065350 | AY498768 | – | – | KM895020 | – |
| <i>Backhousia enata</i> A. J. Ford, Craven & J. Holmes | KC134139 | KC134163 | – | – | – | KC134152 | – |
| <i>Backhousia hughesii</i> C. T. White | KC134140 | KC134164 | – | – | – | KC134153 | – |
| <i>Backhousia kingii</i> Guymer | KC134142 | – | – | – | – | KM895350 | – |
| <i>Backhousia myrtifolia</i> Hook & Harv. | ZF 0266091 | AF368200 | DQ088472 | DQ088408 | – | KC134156 | – |
| <i>Backhousia oligantha</i> A. R. Bean | KC134144 | KM894720 | – | – | – | KM895223 | – |
| <i>Backhousia subargentea</i> (C. T. White) L. A. S. Johnson_ (C. T. White) M. G. Harr. | DQ088409 | AF368202 | DQ088473 | DQ088409 | – | – | – |
| <i>Barongia lophandra</i> P. G. Wilson & B. Hyland | In this study | In this study | In this study | – | – | – | Sankowsky 3890 (K) |
| <i>Beaufortia orbifolia</i> F. Muell | AF048888 | AY521530 | AY498771 | – | – | – | – |
| <i>Blepharocalyx cruckshanksii</i> (Hook. & Arn.) Nied. | JN660857 | AM489978 | MF954437 | JN660956 | AM489895 | AM489814 | – |
| <i>Blepharocalyx salicifolius</i> (Kunth) O. Berg | AY521531 | AY498772 | – | – | AM234084 | – | – |
| <i>Calothamnus validus</i> S. Moore | AF048856 | AF184705 | AY498773 | – | – | – | – |
| <i>Calycolpus moritzianus</i> (O. Berg) Burret | – | – | – | KU945977 | JQ730668 | KU945999 | – |
| <i>Calycorectes bergii</i> Sandwith | MN296376 | – | – | – | – | KX248112 | – |
| <i>Calyptranthes concinna</i> DC. | AM489980 | KP722454 | KU898502 | AM489898 | AM234103 | AM489817 | – |
| <i>Calyptrogenia grandiflora</i> Burret, Notizbl. | MF954024 | – | MF954448 | MF954322 | – | MF954282 | – |
| <i>Campomanesia guazumifolia</i> (Cambess.) O. Berg | AY521532 | AY498777 | – | AM489902 | AM234076 | AM489821 | – |
| <i>Changuava schippii</i> (Standl.) Landrum | MF954027 | GQ981963 | MF954451 | MF954325 | – | GQ982182 | – |
| <i>Cloezia artensis</i> (Montrouz.) P. S. Green | in this study | in this study | in this study | in this study | – | – | McPherson & Munzinger 18155 (MO) |
| <i>Cloezia buxifolia</i> Brongn. & Gris | in this study | in this study | in this study | – | – | – | LowryII, Munzinger & Pignal 6499 (MO) |
| <i>Cloezia floribunda</i> Brongn. & Gris | AF172767 | AY521533 | – | – | AY606255 | – | – |
| <i>Corymbia variegata</i> (F. Muell.) K. D. Hill & L. A. S. Johnson/Corymbiacitriodora (Hook.) K. D. Hill & L. A. S. Johnson | DQ993141 | AF368203 | – | – | DQ352524 | – | – |
| <i>Curitiba prismatica</i> (D. Legrand) Salywon & Landrum | MF954028 | MF954524 | MF954452 | MF954326 | – | MF954286 | – |
| <i>Decaspermum humile</i> (G. Don) A. J. Scott | AY521534 | AY498780 | – | AM489905 | AM234128 | AM489824 | – |
| <i>Eucalyptopsis papuana</i> C. T. White | – | AF368205 | – | – | DQ352538 | AF190371 | – |
| <i>Eucalyptus perriniana</i> F. Muell. exRodway | AM234139 | – | MF954455 | MF954330 | AM489907 | – | – |
| <i>Eugenia adenocalix</i> DC. | MF954042 | – | MF954470 | MF954342 | – | MF954300 | – |

| | | | | | | | |
|--|---------------|---------------|---------------|---------------|-----------|----------|---------------------------|
| <i>Eugenia arenosa</i> Mattos | – | – | – | KJ187658 | JQ033314 | JQ033344 | – |
| <i>Eugenia bimarginata</i> DC. | – | – | – | KJ187664 | KJ187611 | KJ469660 | – |
| <i>Eugenia brevistyla</i> D. Legrand | KJ187614 | MF954460 | MG718641 | – | KJ187667 | KJ469663 | – |
| <i>Eugenia bullata</i> Pancher ex Guillaumin | – | MF954461 | MF954334 | – | MF954034 | MF954292 | – |
| <i>Eugenia bunchosiifolia</i> Nied. | MG707978 | MG718642 | MF954469 | MF954341 | – | – | – |
| <i>Eugenia buxifolia</i> Lam. | KU945987 | KU945992 | In this study | – | KU945979 | KU946000 | Byng 60 (K) |
| <i>Eugenia erythrophylla</i> Strey | JX517830 | – | AY463125. | AY454145. | AY463139 | – | – |
| <i>Eugenia excelsa</i> O. Berg | In this study | In this study | In this study | In this study | KJ187673 | KJ469670 | Byng 66 (K) |
| <i>Eugenia florida</i> DC. | KJ187622 | MG718956 | In this study | MH446205 | KJ187674 | KJ469671 | Mazine 965 (ESA, K) |
| <i>Eugenia lucida</i> Lam. | – | – | AY463110 | AY454132 | AY487289 | – | – |
| <i>Eugenia macrocalyx</i> Mart. ex B. D. Jacks. | JQ626398 | – | – | – | FJ037852 | KX248447 | – |
| <i>Eugenia magnibracteolata</i> Mattos & D. Legrand | KX789271 | MG718650 | – | KX789329 | – | KX789304 | – |
| <i>Eugenia melanogyne</i> (D. Legrand) Sobral | KJ187624 | MG718651 | – | – | KJ187676 | KJ469673 | – |
| <i>Eugenia monticola</i> (Sw.) DC. | MF954037 | KJ012591 | MF954464 | MF954337 | – | MF954295 | – |
| <i>Eugenia myrcianthes</i> Nied. | MG708033 | MG718830 | MF954475 | MF954346 | KU945982 | MH446060 | – |
| <i>Eugenia natalitia</i> Sond. | JX517466 | – | AY463121 | AY454141 | AY463135 | – | – |
| <i>Eugenia neoverrucosa</i> Sobral | – | – | – | KJ187680 | KJ187628 | KJ469676 | – |
| <i>Eugenia oblongata</i> O. Berg | – | – | – | KJ18768 | KJ187630 | KJ469678 | – |
| <i>Eugenia orbiculata</i> Lam. | – | – | AY463111 | KJ187683. | KJ187631 | KJ469679 | – |
| <i>Eugenia paludosa</i> Pancher ex Brongn. & Gris | MF954038 | – | MF954465. | MF954338 | – | MF954296 | – |
| <i>Eugenia pluriflora</i> DC. | KJ187636 | MG718831 | – | – | KJ187688 | KJ469684 | – |
| <i>Eugenia puberula</i> Nied. in H. G. A. Engler & K. A. E. Prantl | KX789282 | – | – | KJ187665 | KJ187612. | KJ469661 | Duarte ESA 85677 (ESA, K) |
| <i>Eugenia pyriformis</i> Cambess. | – | – | In this study | AM489914 | KJ187639 | KJ469687 | Mazine 1028 (ESA, K) |
| <i>Eugenia reinwardtiana</i> (Blume) A. Cunn. ex DC. | KM894685 | – | AY463131 | – | KU945989 | KU946003 | – |
| <i>Eugenia repanda</i> O. Berg | – | In this study | In this study | KJ187692 | KJ187640 | KJ469688 | Lucas 273 (ESA, K) |
| <i>Eugenia roseopetiolata</i> N. Snow & Cable | – | MF954468 | – | – | MF954040 | MF954298 | – |
| <i>Eugenia</i> sp. [AG3] | MN296363 | – | – | MN887414 | – | MN887384 | – |
| <i>Eugenia stipitata</i> McVaugh | MF954043 | – | MF954471 | MF954343 | KJ187698 | MF954301 | – |
| <i>Eugenia subglomerata</i> (Kuntze) Sobral | KJ187626 | KF981335 | – | – | KJ187678 | KJ469674 | – |
| <i>Eugenia subterminalis</i> DC. | MG708058 | MG718958 | – | – | KJ187700 | KJ469696 | – |
| <i>Eugenia sulcata</i> Sping ex Mart. | HM160097 | HM160097 | – | KJ187701 | AM234089 | KJ469697 | – |
| <i>Eugenia tinifolia</i> Lam. | – | – | AY487287 | AY454130 | AY463108. | – | – |
| <i>Eugenia umtamvunensis</i> A. E. Van Wyk | JX517784 | – | AY463128 | AM489911 | AY463142 | – | – |
| <i>Eugenia uniflora</i> L. | DQ088457 | AF21559 | AY463105 | AM489910 | AY487284 | KP719066 | – |
| <i>Eugenia verdoorniae</i> A. E. Van Wyk | JX517398 | – | AY463123.1 | AY454143. | AY463137 | – | – |
| <i>Eugenia verticillata</i> (Vell.) Angely | MG707998 | MG718663 | – | – | KJ187704 | KJ469700 | – |
| <i>Gossia grayi</i> N. Snow & Guymer | JN564152 | – | – | – | AM234132 | KM895411 | – |
| <i>Heteropyxis natalensis</i> Harv. | KM064805 | KM065121 | AY498824 | – | – | – | – |
| <i>Hottea neibensis</i> Alain | MF954046 | – | MF954476 | MF954347 | – | MF954304 | – |
| <i>Kanakomyrtus dawsoniana</i> N. Snow | – | MF954477 | MF954348 | – | HQ225445 | MF954305 | – |
| <i>Legrandia concinna</i> (Phil.) Kausel | AM234072 | AM489990 | MF954478 | – | AM489921 | AM489839 | – |
| <i>Lenwebbia prominens</i> N. Snow & Guymer | MF954048 | KM894619 | – | – | AM234072 | MF954306 | – |
| <i>Lophomyrtus ballata</i> Burret | KM064781 | AM489992 | – | – | AM489923 | AM489841 | – |
| <i>Lophostemon confertus</i> (R. Br.) P. G. Wilson & J. T. Waterh. | AF390444 | AY498794 | AY498794 | AM489925 | AY498794 | – | – |
| <i>Luma apiculata</i> (DC.) Burret | AY498795 | AY498795 | KX789340 | AM489926 | AM234101 | KX789312 | – |
| <i>Lysicarpus angustifolius</i> (Hook.) Druce | – | AF368210 | AY498796 | – | – | – | – |
| <i>Marlierea eugenioides</i> (Cambess.) D. Legrand | AM489996 | HM160099 | – | AM489929 | AM234108 | AM489845 | – |
| <i>Melaleuca viridiflora</i> Sol. ex Gaertn. | AF294611 | AY498798 | – | – | – | EU410242 | – |
| <i>Metrosideros angustifolia</i> (L.) Sm. | KM064919 | KM065077 | – | – | KM064687 | – | – |

| | | | | | | | |
|--|-----------|---------------|---------------|---------------|----------|----------|---------------------------|
| <i>Metrosideros boninensis</i> (Hayata ex Koidz.) Tuyama | AF172734. | In this study | In this study | In this study | – | – | Chase 2455 (K) |
| <i>Metrosideros carminea</i> W. R. B. Oliv. | AF211498 | AY521541 | AY498799 | – | KM064696 | – | – |
| <i>Metrosideros collina</i> (J. R. Forst. & G. Forst.) A. Gray | KM065036 | KM065294 | In this study | EU605584 | AF328068 | – | Christenhusz (TUR, BM) |
| <i>Metrosideros cordata</i> (C. T. White & W. D. Francis) J. W. Dawson | JF950776 | – | In this study | In this study | AY606240 | – | Lucas 27 (K) |
| <i>Metrosideros diffusa</i> (G. Forst.) Sm. | KM064992 | KM065382 | AY498800 | – | – | – | – |
| <i>Metrosideros excelsa</i> Sol. ex Gaertn | JF950777 | KM065270 | AM235426 | AM235462 | AF328052 | – | – |
| <i>Metrosideros macropus</i> Hook. & Arn | AF172745 | AF368212 | AY498801 | EU605503 | AF328047 | – | – |
| <i>Metrosideros nervulosa</i> C. Moore & F. Muell. | DQ088395} | DQ088535 | AY498802 | EU605481 | AF328051 | – | – |
| <i>Metrosideros nitida</i> Brongn. & Gris | AF172770 | In this study | In this study | In this study | – | – | Jérémie & Tirel s. n. (K) |
| <i>Metrosideros operculata</i> Labill. | AF172733 | In this study | In this study | In this study | AY606246 | – | Bamps 6107 |
| <i>Metrosideros polymorpha</i> Gaudich. | – | In this study | In this study | EU605532 | AF328059 | – | Chase 2872 (K) |
| <i>Metrosideros stipularis</i> Griseb. | AF368222 | In this study | In this study | In this study | AM489969 | AM489884 | Cult. RBGE 1995–2370A (E) |
| <i>Mitranthes clarendonensis</i> (Proctor) Proctor | MF954049 | KM065078 | MF954482 | MF954352 | – | – | – |
| <i>Mitranthia bilocularis</i> P. G. Wilson & B. Hyland | AY521543 | In this study | – | In this study | – | – | Sankowsky 3889 |
| <i>Mosiera longipes</i> (O. Berg) Small | MF954051 | – | MF954484 | MF954354 | – | MF954388 | – |
| <i>Myrceugenia myrcioides</i> (Cambess.) O. Berg | – | JN660964 | JN660964 | AM489936 | JN660915 | AM489853 | – |
| <i>Myrcia amazonica</i> DC. | JN091306 | KP722437 | – | JN091267 | JN091214 | JN091405 | – |
| <i>Myrcia bicarinata</i> (O. Berg) D. Legrand | – | KU898370 | – | AM489945 | KU898313 | – | – |
| <i>Myrcia coumete</i> (Aubl.) DC. | AM889731 | – | – | AM489947 | AM234123 | GQ248348 | – |
| <i>Myrcia decorticans</i> DC. | JN091308 | KP722460 | – | JN091273 | KP722383 | KX248905 | – |
| <i>Myrcia flagellaris</i> (D. Legrand) Mattos | HM16009 | KP722430 | MF954360 | – | AM234113 | AM489836 | – |
| <i>Myrcia guianensis</i> (Aubl.) DC. | KJ012690 | – | – | – | JN091277 | JN091415 | – |
| <i>Myrcia laruotteana</i> Cambess. | AM490002 | – | – | AM489939 | AM234115 | AM489856 | – |
| <i>Myrcia multiflora</i> (Lam.) DC. | AM490003 | KP722464 | – | AM489941 | KP722387 | KP722294 | – |
| <i>Myrcia pubipetala</i> Miq. | AM490001 | KP722426 | – | – | AM234114 | AM489855 | – |
| <i>Myrcia rupta</i> M. L. Kawas. & B. K. Holst | AM234124 | AM889732 | – | – | AM489948 | AM489865 | – |
| <i>Myrcia saxatilis</i> (Amshoff) McVaugh | AM490004. | HM160100 | – | AM489943 | AM234119 | AM489860 | – |
| <i>Myrcia selloi</i> (Spreng.) N. Silveira | JN091315 | KP722436 | – | JN091291 | JN091240 | JN091431 | – |
| <i>Myrcia splendens</i> (Sw.) DC. | MF954059 | HM446718 | MF954491 | – | JN091293 | JN091433 | – |
| <i>Myrcianthes fragrans</i> (Sw.) McVaugh | KJ187655 | KJ772955 | AY498803 | – | KJ187708 | KJ469705 | – |
| <i>Myrciaria vexator</i> McVaugh | MF954063 | AY521544 | MF954495 | MF954414 | – | – | – |
| <i>Myrrhimum atropurpureum</i> Schott | MH716442 | MH713607 | MF954496 | MF954415 | – | MF954400 | – |
| <i>Myrtastrum rufopunctatum</i> (Pancher ex Brongn. & Gris) Burret | – | MF954527 | MF954497 | MF954416 | – | MF954401 | – |
| <i>Myrteola nummularia</i> (Lam.) O. Berg | AM234068 | AM490008 | MF954498 | MF954417 | AM489954 | AM489871 | – |
| <i>Myrtus communis</i> L. | AF215593 | AF215593 | KX789342 | AM489955 | AF215628 | KX789314 | – |
| <i>Myrtus nivellei</i> Batt. & Trab. | – | – | – | FJ611325. | GU984339 | HM014143 | – |
| <i>Neomitranthes cordifolia</i> (D. Legrand) D. Legrand | AM489410 | – | – | MF954418 | AM489413 | – | – |
| <i>Neomyrtus pedunculata</i> (Hook. f.) Allan | AM234144 | AM490010 | – | MF954370 | – | – | – |
| <i>Octamyrtus pleiopetala</i> Diels | AM234130 | – | MF954500 | MF954371 | AM489957 | AM489873 | – |
| <i>Osbornia octodonta</i> F. Muell | EF041844 | AY498805 | – | – | – | – | – |
| <i>Pilidiostigma tropicum</i> L. S. Sm. | MF954066 | – | MF954501 | – | – | MF954402 | – |
| <i>Pimenta dioica</i> (L.) Merr. | KM065298 | MF954502 | MF954374. | AM489958 | AM234081 | AM489874 | – |
| <i>Plinia cauliflora</i> (Mart.) O. Berg. | AM234093 | AM490007 | – | NC039395 | AM489952 | AM489869 | – |
| <i>Plinia nana</i> Sobral | MF954068 | – | MF954504 | MF954375 | – | MF954404 | – |
| <i>Psidium cattleyanum</i> Afzel ex | HM160101 | HM160101 | – | AM489962 | AM490014 | AM489878 | – |

| | | | | | | | |
|--|---------------|----------|---------------|---------------|----------|---------------|--------------------|
| Sabine | | | | | | | |
| <i>Psiloxylon mauritianum</i> (BoutonexHook. f.) Baill. | EF026606 | AF368215 | AM235430 | AM235466 | – | – | – |
| <i>Rhodamnia argentea</i> Benth. | AY498810 | AY463132 | AY463132 | – | AF368217 | KM895308 | – |
| <i>Rhodomyrtus macrocarpa</i> Benth. | AY498811 | – | – | AM489965?? | AY525137 | KP095748 | – |
| <i>Ristantia gouldii</i> P. G. Wilson & B. Hyland | In this study | AF368219 | – | In this study | – | – | Sankowsky 3885 (K) |
| <i>Ristantia pachysperma</i> (F. Muell. & F. M. Bailey) P. G. Wilson & J. T. Waterh. | In this study | – | – | In this study | – | – | Sankowsky 3886 (K) |
| <i>Siphoneugena densiflora</i> O. Berg | AM489412 | – | KP722444 | MF954383 | AM489572 | KX789316 | – |
| <i>Sphaerantia chartacea</i> P. G. Wilson & B. Hyland | HM160116/15 | AY521547 | – | In this study | – | – | Sankowsky 3888 (K) |
| <i>Sphaerantia discolor</i> P. G. Wilson & B. Hyland | In this study | – | – | In this study | – | – | Gray 848 (CNS) |
| <i>Stockwellia quadrifida</i> D. J. Carr, S. G. M. Carr & B. Hyland | AY525138 | AY498812 | – | – | DQ352539 | HQ287696 | – |
| <i>Syncarpia glomulifera</i> (Sm.) Nied. | AF368220 | AY498813 | – | – | – | – | – |
| <i>Syzygium acre</i> (Pancher ex Guillaumin) J. W. Dawson | EF026619 | DQ088555 | DQ088480 | DQ088415 | – | – | – |
| <i>Syzygium alatum</i> (Lauterb.) Diels | – | – | In this study | In this study | – | In this study | Barker 115 (K) |
| <i>Syzygium amplifolium</i> L. M. Perry | – | EF026620 | DQ088556 | DQ088481 | – | DQ088416 | – |
| <i>Syzygium angophoroides</i> (F. Muell.) B. Hyland | AY187106 | AY187172 | DQ088557 | – | – | – | – |
| <i>Syzygium anisatum</i> (Vickery) Craven & Biffin | AF368195 | DQ088471 | – | – | M489812 | AM489893 | – |
| <i>Syzygium apodophyllum</i> (F. Muell.) B. Hyland | DQ088558 | DQ088482 | DQ088417 | DQ088417 | – | – | – |
| <i>Syzygium aqueum</i> (Burm. f.) Alston | AY187108 | JF682809 | DQ088559 | DQ088483 | MH826496 | – | – |
| <i>Syzygium arboreum</i> (Baker f.) J. W. Dawson | DQ088560 | DQ088484 | DQ088418 | DQ088418 | – | – | – |
| <i>Syzygium aromaticum</i> (L.) Merr. & L. M. Perry | DQ088561 | DQ088485 | DQ088419 | DQ088419 | – | – | – |
| <i>Syzygium australe</i> (J. C. Wendl. ex Link) B. Hyland | AY187111 | AY187177 | AF368221 | – | KM895253 | – | – |
| <i>Syzygium austrocaledonicum</i> (Seem.) Guillaumin | – | EF026623 | DQ088563 | DQ088486 | – | DQ088420 | – |
| <i>Syzygium brackenridgei</i> (A. Gray) Müll. Stuttg | – | – | DQ088565 | DQ088487 | – | DQ088421 | – |
| <i>Syzygium branderhorstii</i> Lauterb. | AY187115 | AY187181 | DQ088566 | DQ088488 | – | DQ088422 | – |
| <i>Syzygium bullatum</i> (Brongn. & Gris) N. Snow & Byng | DQ088552 | DQ088478 | DQ088413 | – | DQ088552 | – | – |
| <i>Syzygium bungadinnia</i> (F. M. Bailey) B. Hyland | DQ088568 | DQ088490 | DQ088490 | DQ088423. | – | AY187116. | – |
| <i>Syzygium buxifolium</i> Hook. & Arn. | DQ088569 | DQ088491 | DQ088424 | DQ088424 | HQ427087 | – | – |
| <i>Syzygium championii</i> (Benth.) Merr. & L. M. Perry | KP093047 | HQ415318 | – | – | KP095752 | – | – |
| <i>Syzygium claviflorum</i> (Roxb.) Wall. ex A. M. Cowan & Cowan | DQ088546 | DQ088470 | DQ088470 | DQ088406 | – | AY187103 | – |
| <i>Syzygium cordatum</i> Hochst. ex Krauss | EF026625 | JX517332 | DQ088493 | DQ088426 | JQ279706 | – | – |
| <i>Syzygium crebrinerve</i> (C. T. White) L. A. S. Johnson hide S. ramp | EF026627 | DQ088574 | DQ088495 | DQ088428 | KU564625 | – | – |
| <i>Syzygium cumini</i> (L.) Skeels | JX856510 | GU134997 | AY498814 | GQ870669 | GU135395 | – | – |
| <i>Syzygium decussatum</i> (A. C. Sm.) Biffin & Craven | DQ088547 | DQ088474 | DQ088410 | DQ088410 | – | – | – |
| <i>Syzygium fibrosum</i> (F. M. Bailey) T. G. Hartley & L. M. Perry | AY187123 | AY187189 | DQ088577 | DQ088497 | – | DQ088429 | – |
| <i>Syzygium floribundum</i> F. Muell | AY187221 | KM065373 | DQ088531 | DQ088453 | – | AY187155 | – |
| <i>Syzygium francii</i> (Guillaumin) N. Snow, Byng & Munzinger | – | EF026616 | DQ088551 | DQ088477 | – | – | – |
| <i>Syzygium francisii</i> (F. M. Bailey) L. A. S. Johnson | DQ088578 | DQ088498 | DQ088498 | – | KM895364 | – | – |
| <i>Syzygium fullagarii</i> (F. Muell.) Craven | DQ088579 | DQ088499 | DQ088499 | – | – | AY187127. | – |
| <i>Syzygium glenum</i> Craven | AY187096 | AY187162 | DQ088539 | DQ088464 | – | DQ088400 | – |
| <i>Syzygium guineense</i> (Willd.) DC. | EF026628 | DQ088581 | DQ088500 | DQ088432 | – | – | – |
| <i>Syzygium gustavioides</i> (F. M. | AY187128 | AY187194 | DQ088582 | DQ088501 | – | DQ088433 | – |

| | | | | | | | |
|--|---------------|---------------|---------------|---------------|----------|------------|--------------------|
| Bailey) B. Hyland | | | | | | | |
| <i>Syzygium ingens</i> (F. Muell. ex C. Moore) Craven & Biffin | DQ088542 | DQ088466 | DQ088402 | DQ088402 | KM895091 | – | – |
| <i>Syzygium jambos</i> (L.) Alston | JX856511 | GU135056 | KU060786 | DQ088434 | GU135387 | AM489967 | – |
| <i>Syzygium lateriflorum</i> Brongn. & Gris | DQ088585 | DQ088504 | DQ088435 | DQ088435 | – | – | – |
| <i>Syzygium laxeracemosum</i> (Guillaumin) J. W. Dawson | DQ088586 | DQ088506 | DQ088506 | DQ088436 | – | – | – |
| <i>Syzygium luehmannii</i> (F. Muell.) L. A. S. Johnson | AY187197 | DQ088587 | DQ088505 | DQ088437 | AY187131 | KM895401 | – |
| <i>Syzygium macilwraithianum</i> B. Hyland | AY187132 | AY187198 | DQ088588 | DQ088507 | – | – | – |
| <i>Syzygium maire</i> (A. Cunn.) Sykes & Garn. - Jones | EF026632 | DQ088508 | KM065310 | DQ088438 | AM489883 | – | – |
| <i>Syzygium malaccense</i> (L.) Merr. & L. M. Perry | DQ088590 | DQ088509 | – | – | – | – | – |
| <i>Syzygium monimioides</i> Craven | DQ088544 | DQ088468 | DQ088404 | DQ088404 | – | – | – |
| <i>Syzygium moorei</i> (F. Muell.) L. A. S. Johnson | AY187135 | AY187201 | DQ088592 | DQ088510 | – | – | – |
| <i>Syzygium muelleri</i> (Miq.) Miq. | EF026634 | DQ088593 | DQ088511 | DQ088439 | – | – | – |
| <i>Syzygium mulgraveanum</i> (B. Hyland) Craven & Biffin | DQ088622 | DQ088533 | DQ088455 | DQ088455 | – | – | – |
| <i>Syzygium multipetalum</i> Pancher ex Brongn. & Gris | – | EF026635 | DQ088594 | DQ088512 | – | DQ088440 | – |
| <i>Syzygium nervosum</i> A. Cunn. ex DC. | DQ088595 | DQ088513 | DQ088513 | – | – | AY187136 | – |
| <i>Syzygium paniculatum</i> Gaertn. | DQ088598 | DQ088515 | DQ088515 | – | – | AY187138. | – |
| <i>Syzygium pseudofastigiatum</i> B. Hyland | AY187206 | DQ088600 | DQ088516 | – | AY187140 | – | – |
| <i>Syzygium puberulum</i> Merr. & L. M. Perry | DQ088601 | DQ088517 | DQ088517 | – | – | AY187141 | – |
| <i>Syzygium purpureum</i> (L. M. Perry) A. C. Sm. | – | EF026639 | DQ088602 | DQ088518 | – | DQ088442 | – |
| <i>Syzygium pycnanthum</i> Merr. & L. M. Perry | – | EF026640 | DQ088603 | DQ088519 | – | DQ088443 | – |
| <i>Syzygium racemosum</i> (Blume) DC. | – | EF026641 | DQ088604 | DQ088520 | – | DQ088444 | – |
| <i>Syzygium robustum</i> Miq. | – | EF026618 | DQ088553 | DQ088479 | – | DQ088414 | – |
| <i>Syzygium salwinense</i> Merr. & L. M. Perry | KR532640 | GU134997 | DQ088601 | DQ088446 | KR533018 | – | – |
| <i>Syzygium samarangense</i> (Blume) Merr. & L. M. Perry | – | KC815989 | AY525141 | AY498815 | – | – | – |
| <i>Syzygium sayeri</i> (F. Muell.) B. Hyland | DQ088607 | DQ088607 | In this study | – | – | AY187143 | Gadek s. n. (JCT) |
| <i>Syzygium seemannianum</i> Merr. & L. M. Perry | – | EF026642 | DQ088608 | DQ088521 | – | DQ088445 | – |
| <i>Syzygium seemannii</i> (A. Gray) Biffin & Craven | – | EF026613 | DQ088548 | DQ088475 | – | DQ088411 | – |
| <i>Syzygium</i> sp. = [syzy sp. BC 140] | EF026647 | – | DQ088526 | DQ088446 | – | – | – |
| <i>Syzygium stocksii</i> (Duthie) Gamble | KY607864 | KT936460 | – | – | – | – | – |
| <i>Syzygium tetrapterum</i> (Miq.) Chantaran. & J. Parn. | – | EF026649 | DQ088615 | DQ088527 | – | DQ088448 | – |
| <i>Syzygium tierneyanum</i> (F. Muell.) T. G. Hartley & L. M. Perry | AY187147 | AY187213 | DQ088616 | DQ088528 | – | DQ088449 | – |
| <i>Syzygium wesa</i> B. Hyland | DQ088617 | DQ088529 | DQ088529 | DQ088450. | – | AY187150.1 | – |
| <i>Syzygium wilsonii</i> (F. Muell.) B. Hyland | DQ088618 | DQ088530 | DQ088530 | DQ088451 | – | AY187153 | – |
| <i>Thaleropia queenslandica</i> P. J. Wilson | AF368223 | DQ088460 | DQ088397 | DQ088397 | – | – | – |
| <i>Tristania neriifolia</i> (Sims) R. Br. | AF368224 | DQ088461 | AY498817 | DQ088398 | – | – | – |
| <i>Tristaniopsis anomala</i> (Merr.) P. G. Wilson & J. T. Waterh. | In this study | In this study | – | – | – | – | S.100612 (SAN) |
| <i>Tristaniopsis beccarii</i> (Ridl.) P. G. Wilson & J. T. Waterh. | In this study | In this study | In this study | In this study | – | – | Berhamen 727 (SAN) |
| <i>Tristaniopsis collina</i> P. G. Wilson & J. T. Waterh. | In this study | KM894817 | In this study | – | – | – | NSW.210020 (SAN) |
| <i>Tristaniopsis exiliflora</i> (F. Muell.) P. G. Wilson & J. T. Waterh. | – | EF173072 | – | – | – | – | – |
| <i>Tristaniopsis laurina</i> (Sm.) P. G. | – | AF184710 | AY498818 | – | – | – | – |

| | | | | | | | |
|--|---------------|---------------|---------------|---------------|----------|----------|------------------------|
| Wilson & J. T. Waterh. | | | | | | | |
| <i>Tristaniaopsis whiteana</i> (Griff.) P. G. Wilson & J. T. Waterh. | In this study | In this study | In this study | In this study | - | - | Berhamen 778 (SAN) |
| <i>Ugni molinae</i> Turcz. | AY498819 | Y498819 | MF954384 | AM489970 | AM490018 | AM489885 | - |
| <i>Uromyrtus emarginata</i> (Pancher ex Baker f.) Burret | MF954077 | MF954529 | MF954514 | MF954385 | - | MF954413 | - |
| <i>Xanthomyrtus compacta</i> Diels | AM234148. | - | MF954515 | MF954386 | AM489972 | AM489887 | - |
| <i>Xanthomyrtus flavida</i> (Stapf) Diels | In this study | In this study | In this study | In this study | - | - | Wilson SAN152562 (SAN) |
| <i>Xanthomyrtus montivaga</i> A. J. Scott | AM234147 | - | MF954516 | MF954387 | AM489971 | AM489886 | - |
| <i>Xanthostemon chrysanthus</i> (F. Muell.) Benth. | AF368227 | EU410135 | - | - | - | - | - |

S3 - Fruit type reported for each species

| Taxa | Fruit Type with reference |
|---|--|
| <i>Algrizea macrochlamys</i> (DC.) Proença & Nic Lugh. | fleshy/drupe (https://www.jstor.org/) |
| <i>Archirhodomyrtus turbinata</i> (Schltr.) Burret | fleshy/berry (https://en.wikipedia.org/) |
| <i>Backhousia angustifolia</i> F. Muell | dry/capsule (researchgate.net/publication/271078147) |
| <i>Campomanesia guazumifolia</i> (Cambess.) O. Berg | fleshy/berry (https://www.scielo.br/scielo.php) |
| <i>Chamguava schippii</i> (Standl.) Landrum | fleshy/berry (https://stricollections.org/portal/taxa/index.php) |
| <i>Cloezia artensis</i> (Montrouz.) P. S. Green | dry/capsule (http://endemia.nc/) |
| <i>Eucalyptus perriniana</i> F. Muell. exRodway | dry/capsule (http://keyserver.lucidcentral.org/https://vicflora.rbg.vic.gov.au/) |
| <i>Eugenia arenosa</i> Mattos | fleshy/ berry (https://www.researchgate.net/publication/326465558) |
| <i>Eugenia brevistyla</i> D. Legrand | fleshy/drupe (https://www.earth.com/https://bioone.org/journals/Systematic - Botany/vol - 37) |
| <i>Eugenia bullata</i> Pancher ex Guillaumin =Eug. Ro | fleshy/ berry (http://endemia.nc/) |
| <i>Eugenia florida</i> DC. | fleshy/drupe (http://tropical.theferns.info/) |
| <i>Eugenia lucida</i> Lam. | fleshy/drupe (https://plants.jstor.org/compilation/) |
| <i>Eugenia macrocalyx</i> Mart. ex B. D. Jacks. | fleshy/drupe (https://www.researchgate.net/publication/304008230) |
| <i>Eugenia monticola</i> (Sw.) DC. | fleshy/berry (https://www.researchgate.net/) |
| <i>Eugenia natalitia</i> Sond. | fleshy/berry (https://www.zimbabweflora.co.zw/) |
| <i>Eugenia neoverrucosa</i> Sobral | fleshy/drupe (https://www.scielo.br/pdf/bn/v11n1/19.pdf) |
| <i>Eugenia orbiculata</i> Lam. | fleshy/berry (http://pages.intnet.mu/nathraj/eugor.html) |
| <i>Eugenia paludosa</i> Pancher ex Brongn. & Gris | fleshy/drupe (https://endemia.nc/flore/fiche4223) |
| <i>Eugenia puberula</i> Nied. in Engler & Prantl | flashy/drupe (https://teses.usp.br/) |
| <i>Eugenia reinwardtiana</i> (Blume) A. Cunn. ex DC. | flashy/drupe (https://cnas - re. uog. edu/) |
| <i>Eugenia repanda</i> O. Berg | flashy/drupe (http://tropical.theferns.info/) |
| <i>Eugenia sulcata</i> Sping ex Mart. | fleshy/berry rounded (http://www.bananasraras.org/) |
| <i>Eugenia umtamvunensis</i> A. E. Van Wyk | fleshy/drupe (https://core.ac.uk/download/pdf/81992013.pdf) |
| <i>Eugenia uniflora</i> L. | fleshy/drupe (http://www.iucngisd.org/) |
| <i>Eugenia verticillata</i> (Vell.) Angely | fleshy/drupe (http://tropical.theferns.info/viewtropical.php) |
| <i>Eugenia verdoorniae</i> A. E. van Wyk | fleshy/ berry (https://inaturalist.nz/taxa/192144) |
| <i>Heteropyxis natalensis</i> Harv. | dry/capsule (http://pza.sanbi.org/) |
| <i>Hottea neibensis</i> Alain | fleshy/drupe (https://www.sciencedirect.com/science/article/pii/S1055790317300052) |
| <i>Legrandia concinna</i> (Phil.) Kausel | flehy/drupe (https://treesandshrubsonline.org/) |
| <i>Luma apiculata</i> (DC.) Burret | flehy/berry (Mora2017. pdf) |
| <i>Lysicarpus angustifolius</i> (Hook.) Druce | dry/ capsule (http://www.npqtownsville.org.au/) |
| <i>Metrosideros angustifolia</i> (L.) Sm. | dry/woody casule (https://en.wikipedia.org/http://pza.sanbi.org/https://treesa.org/) |
| <i>Metrosideros operculata</i> Labill. | dry/capsule (https://www.repository.naturalis.nl/document/565561) |
| <i>Metrosideros polymorpha</i> Gaudich. | dry/capsule (https://en.wikipedia.org/http://nativeplants.hawaii.edu/) |
| <i>Metrosideros stipularis</i> Griseb. Ex tepualia | dry/capsule (Wilson 2011) |
| <i>Mosiera longipes</i> (O. Berg) Small | flehy/berry (https://books.google.it/) |
| <i>Myrceugenia myrcioides</i> (Cambess.) O. Berg | flehy/drupe (https://www.scielo.br/pdf/bn/v11n1/19.pdf) |
| <i>Myrcia decorticans</i> DC. | hairy fleshy (www.biotaxa.org) |
| <i>Myrtus communis</i> L. | fleshy/berry (https://besjournals.onlinelibrary.wiley.com) |
| <i>Neomyrtus pedunculata</i> (Hook. f.) Allan | fleshy/berry (https://www.nzpcn.org.nz/) |
| <i>Osbornia octodonta</i> F. Muell | Fleshy/drupe (https://books.google.it/) |
| <i>Psidium cattleianum</i> Sabine | fleshy/berry (https://www.cabi.org/) |
| <i>Psiloxylon mauritianum</i> (BoutonexHook. f.) Baill. | fleshy/berry (https://fr.wikipedia.org/https://www.ncbi.nlm.nih.gov/pmc) |
| <i>Syzygium acre</i> (Pancher ex Guillaumin) J. W. Dawson | fleshy/drupe (http://endemia.nc/) |
| <i>Syzygium alatum</i> (Lauterb.) Diels | fleshy/drupe (http://tropical.theferns.info/) |

| | |
|---|--|
| <i>Syzygium angophoroides</i> (F. Muell.) B. Hyland | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium anisatum</i> (Vickery) Craven & Biffin | dry/dry papery capsules (http://tropical.theferns.info/) |
| <i>Syzygium arboreum</i> (Baker f.) J. W. Dawson | flashy /drupe (http://endemia.nc/) |
| <i>Syzygium australe</i> (J. C. Wendl. ex Link) B. Hyland | fleshy/drupe (http://tropical.theferns.info/) |
| <i>Syzygium austrocaledonicum</i> (Seem.) Guillaumin | fleshy/drupe (http://endemia.nc/) |
| <i>Syzygium fibrosum</i> (F. M. Bailey) T. G. Hartley & L. M. Perry | fleshy/drupe (http://tropical.theferns.info/) |
| <i>Syzygium floribundum</i> F. Muell | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium francii</i> (Guill.) N. Snow, Byng & Munzinger | flesh/drupe (http://endemia.nc/) |
| <i>Syzygium francisii</i> (F. M. Bailey) L. A. S. Johnson | flashy/drupe drysh flesh (http://www.anbg.gov.au/) |
| <i>Syzygium fullagarii</i> (F. Muell.) Craven | fleshy/berry (Craven and Biffin 2010) |
| <i>Syzygium guineense</i> (Willd.) DC. | dry /subwoody drupe (http://pza.sanbi.org/) |
| <i>Syzygium jambos</i> (L.) Alston | fleshy/drupe (http://www.efloras.org/) |
| <i>Syzygium luehmannii</i> (F. Muell.) L. A. S. Johnson | fleshy/drupe (https://books.google.it/) |
| <i>Syzygium macilwraithianum</i> B. Hyland | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium malaccense</i> (L.) Merr. & L. M. Perry | fleshy/drupe (http://tropical.theferns.info/) |
| <i>Syzygium monimioides</i> Craven | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium moorei</i> (F. Muell.) L. A. S. Johnson | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium nervosum</i> A. Cunn. ex DC. | fleshy/drupe (https://books.google.it/) |
| <i>Syzygium pseudofastigiatum</i> B. Hyland | fleshy/drupe (http://www.anbg.gov.au/) |
| <i>Syzygium purpureum</i> (L. M. Perry) A. C. Sm. | fleshy/berry (Craven and Biffin 2010) |
| <i>Syzygium pycnanthum</i> Merr. & L. M. Perry | fleshy/drupe (http://tropical.theferns.info/) |
| <i>Syzygium robustum</i> Miq. | flashy/drupe (https://www.earth.com/) |
| <i>Syzygium seemannii</i> (A. Gray) Biffin & Craven | flashy/berry (Craven and Biffin 2010) |
| <i>Syzygium tetrapterum</i> (Miq.) Chantaran. & J. Parn. | flashy/drupe (Craven and Biffin 2010) |
| <i>Thaleropia queenslandica</i> P. J. Wilson | dry/ capsule (http://www.anbg.gov.au/) |
| <i>Tristaniopsis anomala</i> (Merr.) P. G. Wilson & J. T. Waterh. | dry/ capsule (Wilson 2011) |
| <i>Ugni molinae</i> Turcz. | fleshy/berry (https://www.nzpcn.org.nz/flora/species) |
| <i>Xanthomyrtus montivaga</i> A. J. Scott | fleshy/berry (https://books.google.it/) |
| <i>Xanthostemon chrysanthus</i> (F. Muell.) Benth. | dry/capsule (http://www.anbg.gov.au/) |

S4 - Comparison of BKMMST phylogenetic tree in latest studies

